

Page 11, line 31, after "(rat GRR3)" insert --(SEQ ID NO: 42)--.

Page 12, line 1, after "sequence" insert --(SEQ ID NO: 43)--.

Page 12, line 25, after "consensus sequence" insert --(SEQ ID NO: 44)--.

Page 98, line 18, after "Figure 26" insert --(SEQ ID NO: 44)--.

Page 98, line 30, after "Figure 26" insert --(SEQ ID NO: 44)--.

REMARKS

As described above, the specification has been amended so that the figures are more clearly referenced by the appropriate sequence identification numbers. The amendments are fully supported by the specification, and no new matter has been added.

Respectfully submitted,



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Dept. 430, M/S 27-4-A
AMGEN INC.
One Amgen Center Drive
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Fox, Gary M
Jing, Shuqian
Wen, Duanzhi
- (ii) TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTORS
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: AMGEN INC
(B) STREET: One Amgen Center Drive
(C) CITY: Thousand Oaks
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/866,354
(B) FILING DATE: 30-MAY-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/837,199
(B) FILING DATE: 14-APR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/015,907
(B) FILING DATE: 22-APR-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/017,221
(B) FILING DATE: 09-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Curry, Daniel R.
(B) REGISTRATION NUMBER: 32,727
(C) REFERENCE/DOCKET NUMBER: A-401B

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2568 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 540..1934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA	ACATCCCTAA	60
CGAGCATCCG	AGCCGAGGGC	TCTGCTCGGA	AATCGTCCTG	GCCCAACTCG	GCCCTTCGAG	120
CTCTCGAAGA	TTACCGCATC	TATTTTTTTT	TTCTTTTTTT	TCTTTTCCTA	GCGCAGATAA	180
AGTGAGCCCG	GAAAGGGAAG	GAGGGGGCGG	GGACACCATT	GCCCTGAAAG	AATAAATAAG	240
TAAATAAACA	AACTGGCTCC	TCGCCGCAGC	TGGACGCGGT	CGGTTGAGTC	CAGGTTGGGT	300
CGGACCTGAA	CCCCTAAAAG	CGGAACCGCC	TCCCGCCCTC	GCCATCCCGG	AGCTGAGTCG	360
CCGGCGGCGG	TGGCTGCTGC	CAGACCCGGA	GTTTCCTCTT	TCACTGGATG	GAGCTGAACT	420
TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	480
GACCCAGCGG	CGGCTCGGGA	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCGC	GCCGGCACC	539
ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC	Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu	1 5 10 15	587			
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC	Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala	20 25 30	635			
AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG	Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr	35 40 45	683			
CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC	Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser	50 55 60	731			
GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG	Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys	65 70 75 80	779			
CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG	Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu	85 90 95	827			
AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA	Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly	100 105 110	875			
AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG	Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu	115 120 125	923			
TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA	Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln	130 135 140	971			
GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC	Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala	145 150 155 160	1019			
TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC	Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr		1067			

				165				170				175					
CCG	TGC	ACC	ACC	AGC	GTG	TCC	AAC	GAT	GTC	TGC	AAC	CGC	CGC	AAG	TGC	1115	
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys		
180				185				190									
CAC	AAG	GCC	CTC	CGG	CAG	TTC	TTT	GAC	AAG	GTC	CCG	GCC	AAG	CAC	AGC	1163	
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser		
195				200				205									
TAC	GGA	ATG	CTC	TTC	TGC	TCC	TGC	CGG	GAC	ATC	GCC	TGC	ACA	GAG	CGG	1211	
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg		
210				215				220									
AGG	CGA	CAG	ACC	ATC	GTG	CCT	GTG	TGC	TCC	TAT	GAA	GAG	AGG	GAG	AAG	1259	
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys		
225				230				235				240					
CCC	AAC	TGT	TTG	AAT	TTG	CAG	GAC	TCC	TGC	AAG	ACG	AAT	TAC	ATC	TGC	1307	
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys		
245				250				255				260					
AGA	TCT	CGC	CTT	GCG	GAT	TTT	TTT	ACC	AAC	TGC	CAG	CCA	GAG	TCA	AGG	1355	
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg		
260				265				270				275					
TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	GCT	GAC	TGC	CTC	CTC	GCC	1403	
Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala		
275				280				285				290					
TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	CCC	AAC	TAC	ATA	GAC	TCC	1451	
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser		
290				295				300									
AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	TGC	AGC	AAC	AGT	GGG	AAC	1499	
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn		
305				310				315				320					
GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	TTC	TTC	AAG	GAC	AAT	ACA	1547	
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr		
325				330				335				340					
TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	AAT	GGC	TCC	GAT	GTG	ACC	1595	
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr		
340				345				350				355					
GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	ACC	ACT	GCC	ACT	ACC	ACC	1643	
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr		
355				360				365				370					
ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	GGG	CCA	GCA	GGG	TCT	GAG	1691	
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu		
370				375				380				385					
AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	TGT	GCA	AAT	TTA	CAG	GCA	1739	
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala		
385				390				395				400					
CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGC	AAT	ACA	CAC	CTC	TGT	ATT	TCC	1787	
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser		
405				410				415				420					
AAT	GGT	AAT	TAT	GAA	AAA	GAA	GGT	CTC	GGT	GCT	TCC	AGC	CAC	ATA	ACC	1835	
Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr		

420	425	430	
ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG			1883
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu			
435	440	445	
GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA			1931
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr			
450	455	460	
TCA TAGCTGCATT AAAAAAATAC AATATGGACA TGTA AAAAAGA CAAAAACCAA			1984
Ser			
465			
GTTATCTGTT TCCTGTTCTC TTGTATAGCT GAAATTCCAG TTTAGGAGCT CAGTTGAGAA			2044
ACAGTTCCAT TCAACTGGAA CATT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT			2104
TTNGGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC AAATCAGAA GGCTTTGGGA			2164
TATGCTGTAT TTAAAGGGA CAGTTTGTA CTTGGGCTGT AAAGCAAACCT GGGGCTGTGT			2224
TTTCGATGAT GATGATNATC ATGATNATGA TNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN			2284
NNNNNNNNNN GATTTTAACA GTTTTACTTC TGGCCTTTCC TAGCTAGAGA AGGAGTTAAT			2344
ATTTCTAAGG TAACTCCCAT ATCTCCTTTA ATGACATTGA TTTCTAATGA TATAAATTTT			2404
AGCCTACATT GATGCCAAGC TTTTTTGCCA CAAAGAAGAT TCTTACCAAG AGTGGGCTTT			2464
GTGGAACAG CTGGTACTGA TGTTACCTT TATATATGTA CTAGCATTTT CCACGCTGAT			2524
GTTTATGTAC TGTAACAGT TCTGCACTCT TGTACAAAAG AAAA			2568

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu
1				5					10					15	
Leu	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala
		20						25					30		
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr
		35					40					45			
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Ala	Ser
	50					55					60				
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys
65					70					75					80
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu
			85						90					95	

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
 355 360 365
 Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
 370 375 380
 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
 385 390 395 400
 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
 405 410 415
 Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
 420 425 430
 Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu

435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
 450 455 460

Ser
 465

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 302..1705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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AGCTCGCTCT CCCGGGGCAG TGGTGTGGAT GCACCGGAGT TCGGGCGCTG GGCAAGTTGG      60
GTCGGAAC TG AACCCCTGAA AGCGGGTCCG CCTCCCGCCC TCGCGCCCGC CCGGATCTGA      120
GTCGCTGGCG GCGGTGGGCG GCAGAGCGAC GGGGAGTCTG CTCTCACCTT GGATGGAGCT      180
GAACTTTGAG TGGCCAGAGG AGCGCAGTCG CCCGGGGGATC GCTGCACGCT GAGCTCTCTC      240
CCCAGAGACCG GCGGCGGGCT TTGGATTTTG GGGGGGCGGG GACCAGCTGC GCGGCGGCAC      300
C ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA CTC CTG GAT TTG      346
  Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu
    1             5             10             15

CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG GAC TGT GTG AAA      394
Leu Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys
           20             25             30

GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC ACC AAG TAC CGC      442
Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg
           35             40             45

ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC TTC AGC CTG ACA      490
Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr
           50             55             60

TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC ATG GAG GCC TTG      538
Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu
           65             70             75

AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG GGC ATG AAG AAA      586
Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys
           80             85             90             95

GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC CAG AGC CTG CAG      634
Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln
           100            105            110

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GGA Gly	AAT Asn	GAC Asp	CTC Leu 115	CTG Leu	GAA Glu	GAT Asp	TCC Ser	CCG Pro 120	TAT Tyr	GAG Glu	CCG Pro	GTT Val	AAC Asn 125	AGC Ser	AGG Arg	682
TTG Leu	TCA Ser	GAT Asp 130	ATA Ile	TTC Phe	CGG Arg	GCA Ala	GTC Val 135	CCG Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTC Phe	CAG Gln	730
CAA Gln	GTG Val 145	GAA Glu	CAC His	ATT Ile	TCC Ser	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAC Asp	GCA Ala	GCC Ala	AAG Lys	778
GCC Ala 160	TGC Cys	AAC Asn	CTG Leu	GAC Asp	GAC Asp 165	ACC Thr	TGT Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCC Ala	TAC Tyr	ATC Ile 175	826
ACC Thr	CCC Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	ATG Met	TCC Ser	AAC Asn	GAG Glu 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGT Arg 190	AAG Lys	874
TGC Cys	CAC His	AAG Lys	GCC Ala 195	CTC Leu	AGG Arg	CAG Gln	TTC Phe 200	TTC Phe	GAC Asp	AAG Lys	GTT Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	922
AGC Ser	TAC Tyr	GGG Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACC Thr	GAG Glu	970
CGG Arg	CGG Arg 225	CGA Arg	CAG Gln	ACT Thr	ATC Ile	GTC Val 230	CCC Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAA Glu	CGA Arg	GAG Glu	1018
AGG Arg 240	CCC Pro	AAC Asn	TGC Cys	CTG Leu	AGT Ser 245	CTG Leu	CAA Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACC Thr	AAT Asn	TAC Tyr	ATC Ile 255	1066
TGC Cys	AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCA Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	1114
AGG Arg	TCT Ser	GTC Val	AGC Ser 275	AAC Asn	TGT Cys	CTT Leu	AAG Lys	GAG Glu 280	AAC Asn	TAC Tyr	GCA Ala	GAC Asp	TGC Cys 285	CTC Leu	CTG Leu	1162
GCC Ala	TAC Tyr	TCG Ser 290	GGA Gly	CTG Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACT Thr	CCC Pro	AAC Asn 300	TAC Tyr	GTA Val	GAC Asp	1210
TCC Ser	AGC Ser 305	AGC Ser	CTC Leu	AGC Ser	GTG Val	GCA Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGC Ser	GGC Gly	1258
AAT Asn 320	GAC Asp	CTG Leu	GAA Glu	GAC Asp	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	CTG Leu	AAT Asn 330	TTT Phe	TTT Phe	AAG Lys	GAC Asp	AAT Asn 335	1306
ACT Thr	TGT Cys	CTC Leu	AAA Lys 340	AAT Asn	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCA Ser	GAT Asp 350	GTG Val	1354
ACC Thr	ATG Met	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	CCT Pro	CCA Pro	GTC Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACC Thr	ACT Thr	1402

ACC	ACT	GCC	TTC	CGG	GTC	AAG	AAC	AAG	CCT	CTG	GGG	CCA	GCA	GGG	TCT	1450
Thr	Thr	Ala	Phe	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	
		370					375					380				
GAG	AAT	GAG	ATC	CCC	ACA	CAC	GTT	TTA	CCA	CCC	TGT	GCG	AAT	TTG	CAG	1498
Glu	Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	
	385					390					395					
GCT	CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGT	AGC	ACA	CAC	CTC	TGT	CTT	1546
Ala	Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Ser	Thr	His	Leu	Cys	Leu	
400					405				410						415	
TCT	GAT	AGT	GAT	TTC	GGA	AAG	GAT	GGT	CTC	GCT	GGT	GCC	TCC	AGC	CAC	1594
Ser	Asp	Ser	Asp	Phe	Gly	Lys	Asp	Gly	Leu	Ala	Gly	Ala	Ser	Ser	His	
				420					425					430		
ATA	ACC	ACA	AAA	TCA	ATG	GCT	GCT	CCT	CCC	AGC	TGC	AGT	CTG	AGC	TCA	1642
Ile	Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Ser	Leu	Ser	Ser	
			435					440					445			
CTG	CCG	GTG	CTG	ATG	CTC	ACC	GCC	CTT	GCT	GCC	CTG	TTA	TCT	GTA	TCG	1690
Leu	Pro	Val	Leu	Met	Leu	Thr	Ala	Leu	Ala	Ala	Leu	Leu	Ser	Val	Ser	
		450					455					460				
TTG	GCA	GAA	ACG	TCG	TAGCTGCATC	CGGGAAAACA	GTATGAAAAG	ACAAAAGAGA								1745
Leu	Ala	Glu	Thr	Ser												
	465															
ACCAAGTATT	CTGTCCCTGT	CCTCTTGTAT	ATCTGAAAAT	CCAGTTTTAA	AAGCTCCGTT											1805
GAGAAGCAGT	TTCACCCAAC	TGGAACTCTT	TCCTTGTTTT	TAAGAAAGCT	TGTGGCCCTC											1865
AGGGGCTTCT	GTTGAAGAAC	TGCTACAGGG	CTAATTCCAA	ACCCATAAGG	CTCTGGGGCG											1925
TGGTGCGGCT	TAAGGGGACC	ATTTGCACCA	TGTAAAGCAA	GCTGGGCTTA	TCATGTGTTT											1985
GATGGTGAGG	ATGGTAGTGG	TGATGATGAT	GGTAATTTTA	ACAGCTTGAA	CCCTGTTCTC											2045
TCTACTGGTT	AGGAACAGGA	GATACTATTG	ATAAAGATTC	TTCCATGTCT	TACTCAGCAG											2105
CATTGCCTTC	TGAAGACAGG	CCCGCAGCCG	TCG													2138

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu	
1				5					10					15		
Met	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala	
		20						25					30			
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	
		35					40					45				
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Thr	Ser	

50					55					60					
Gly 65	Leu	Glu	Ala	Lys	Asp 70	Glu	Cys	Arg	Ser	Ala 75	Met	Glu	Ala	Leu	Lys 80
Gln	Lys	Ser	Leu	Tyr 85	Asn	Cys	Arg	Cys	Lys 90	Arg	Gly	Met	Lys	Lys 95	Glu
Lys	Asn	Cys	Leu 100	Arg	Ile	Tyr	Trp	Ser 105	Met	Tyr	Gln	Ser	Leu 110	Gln	Gly
Asn	Asp	Leu 115	Leu	Glu	Asp	Ser	Pro 120	Tyr	Glu	Pro	Val	Asn 125	Ser	Arg	Leu
Ser	Asp 130	Ile	Phe	Arg	Ala	Val 135	Pro	Phe	Ile	Ser	Asp 140	Val	Phe	Gln	Gln
Val 145	Glu	His	Ile	Ser	Lys 150	Gly	Asn	Asn	Cys	Leu 155	Asp	Ala	Ala	Lys	Ala 160
Cys	Asn	Leu	Asp	Asp 165	Thr	Cys	Lys	Lys	Tyr 170	Arg	Ser	Ala	Tyr	Ile 175	Thr
Pro	Cys	Thr	Thr 180	Ser	Met	Ser	Asn	Glu 185	Val	Cys	Asn	Arg	Arg 190	Lys	Cys
His	Lys	Ala 195	Leu	Arg	Gln	Phe	Phe 200	Asp	Lys	Val	Pro	Ala 205	Lys	His	Ser
Tyr	Gly 210	Met	Leu	Phe	Cys	Ser 215	Cys	Arg	Asp	Ile	Ala 220	Cys	Thr	Glu	Arg
Arg 225	Arg	Gln	Thr	Ile	Val 230	Pro	Val	Cys	Ser	Tyr 235	Glu	Glu	Arg	Glu	Arg 240
Pro	Asn	Cys	Leu	Ser 245	Leu	Gln	Asp	Ser	Cys 250	Lys	Thr	Asn	Tyr	Ile 255	Cys
Arg	Ser	Arg	Leu 260	Ala	Asp	Phe	Phe 265	Thr	Asn	Cys	Gln	Pro	Glu 270	Ser	Arg
Ser	Val	Ser 275	Asn	Cys	Leu	Lys	Glu 280	Asn	Tyr	Ala	Asp	Cys 285	Leu	Leu	Ala
Tyr	Ser 290	Gly	Leu	Ile	Gly	Thr 295	Val	Met	Thr	Pro	Asn 300	Tyr	Val	Asp	Ser
Ser 305	Ser	Leu	Ser	Val	Ala 310	Pro	Trp	Cys	Asp	Cys 315	Ser	Asn	Ser	Gly	Asn 320
Asp	Leu	Glu	Asp	Cys 325	Leu	Lys	Phe	Leu	Asn 330	Phe	Phe	Lys	Asp	Asn 335	Thr
Cys	Leu	Lys	Asn 340	Ala	Ile	Gln	Ala	Phe 345	Gly	Asn	Gly	Ser	Asp 350	Val	Thr
Met	Trp	Gln 355	Pro	Ala	Pro	Pro	Val 360	Gln	Thr	Thr	Thr	Ala 365	Thr	Thr	Thr
Thr	Ala 370	Phe	Arg	Val	Lys	Asn 375	Lys	Pro	Leu	Gly	Pro 380	Ala	Gly	Ser	Glu
Asn 385	Glu	Ile	Pro	Thr	His 390	Val	Leu	Pro	Pro	Cys 395	Ala	Asn	Leu	Gln	Ala 400

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..539

(D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of

Figure 5 Gdnfr"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 540..1937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATCTGGCCT	CGGAACACGC	CATTCTCCGC	GCCGCTTCCA	ATAACCACTA	ACATCCCTAA		60
CGAGCATCCG	AGCCGAGGGC	TCTGTCGGA	AATCGTCCTG	GCCCAACTCG	GCCCTTCGAG		120
CTCTCGAAGA	TTACCGCATC	TATTTTTTTT	TTCTTTTTTT	TCTTTTCCTA	GCGCAGATAA		180
AGTGAGCCCG	GAAAGGGAAG	GAGGGGGCGG	GGACACCATT	GCCCTGAAAG	AATAAATAAG		240
TAAATAAACA	AACTGGCTCC	TCGCCGCAGC	TGGACGCGGT	CGGTTGAGTC	CAGGTTGGGT		300
CGGACCTGAA	CCCCTAAAAG	CGGAACCGCC	TCCCGCCCTC	GCCATCCCCG	AGCTGAGTCG		360
CCGGCGGCGG	TGGCTGCTGC	CAGACCCGGA	GTTTCCTCTT	TCACTGGATG	GAGCTGAACT		420
TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA		480
GACCCAGCGG	CGGCTCGGGA	TTTTTTTGGG	GGGGCGGGGA	CCAGCCCCGC	GCCGGCACC		539
ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC							587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu							
1 5 10 15							
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC							635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala							

20				25				30								
AGT Ser	GAT Asp	CAG Gln 35	TGC Cys	CTG Leu	AAG Lys	GAG Glu	CAG Gln 40	AGC Ser	TGC Cys	AGC Ser	ACC Thr	AAG Lys 45	TAC Tyr	CGC Arg	ACG Thr	683
CTA Leu	AGG Arg 50	CAG Gln	TGC Cys	GTG Val	GCG Ala	GGC Gly 55	AAG Lys	GAG Glu	ACC Thr	AAC Asn	TTC Phe 60	AGC Ser	CTG Leu	GCA Ala	TCC Ser	731
GGC Gly 65	CTG Leu	GAG Glu	GCC Ala	AAG Lys	GAT Asp 70	GAG Glu	TGC Cys	CGC Arg	AGC Ser	GCC Ala 75	ATG Met	GAG Glu	GCC Ala	CTG Leu	AAG Lys 80	779
CAG Gln	AAG Lys	TCG Ser	CTC Leu	TAC Tyr 85	AAC Asn	TGC Cys	CGC Arg	TGC Cys	AAG Lys 90	CGG Arg	GGT Gly	ATG Met	AAG Lys	AAG Lys 95	GAG Glu	827
AAG Lys	AAC Asn	TGC Cys	CTG Leu 100	CGC Arg	ATT Ile	TAC Tyr	TGG Trp	AGC Ser 105	ATG Met	TAC Tyr	CAG Gln	AGC Ser	CTG Leu 110	CAG Gln	GGA Gly	875
AAT Asn	GAT Asp	CTG Leu 115	CTG Leu	GAG Glu	GAT Asp	TCC Ser	CCA Pro 120	TAT Tyr	GAA Glu	CCA Pro	GTT Val	AAC Asn 125	AGC Ser	AGA Arg	TTG Leu	923
TCA Ser 130	GAT Asp	ATA Ile	TTC Phe	CGG Arg	GTG Val	GTC Val 135	CCA Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTT Phe	CAG Gln	CAA Gln	971
GTG Val 145	GAG Glu	CAC His	ATT Ile	CCC Pro	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAT Asp	GCA Ala	GCG Ala	AAG Lys	GCC Ala 160	1019
TGC Cys	AAC Asn	CTC Leu	GAC Asp 165	GAC Asp	ATT Ile	TGC Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCG Ala	TAC Tyr	ATC Ile 175	ACC Thr	1067
CCG Pro	TGC Cys	ACC Thr 180	ACC Thr	AGC Ser	GTG Val	TCC Ser	AAN Xaa 185	GAT Asp	GTC Val	TGC Cys	AAC Asn	CGC Arg 190	CGC Arg	AAG Lys	TGC Cys	1115
CAC His	AAG Lys 195	GCC Ala	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1163
TAC Tyr 210	GGA Gly	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1211
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1259
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC Ile 255	TGC Cys	1307
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe 265	ACC Thr	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1355
TCT Ser	GTC Val	AGC Ser	AGC Ser	TGT Cys	CTA Leu	AAG Lys	GAA Glu	AAC Asn	TAC Tyr	GCT Ala	GAC Asp	TGC Cys	CTC Leu	CTC Leu	GCC Ala	1403

275												280				285				
TAC Tyr	TCG Ser 290	GGG Gly	CTT Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACC Thr	CCC Pro	AAC Asn 300	TAC Tyr	ATA Ile	GAC Asp	TCC Ser	1451				
AGT Ser 305	AGC Ser	CTC Leu	AGT Ser	GTG Val	GCC Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGT Ser	GGG Gly	AAC Asn 320	1499				
GAC Asp	CTA Leu	GAA Glu	GAG Glu	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	TTG Leu	AAT Asn 330	TTC Phe	TTC Phe	AAG Lys	GAC Asp	AAT Asn 335	ACA Thr	1547				
TGT Cys	CTT Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCC Ser	GAT Asp 350	GTG Val	ACC Thr	1595				
GTG Val	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	TTC Phe	CCA Pro	GTA Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACT Thr	ACC Thr	ACC Thr	1643				
ACT Thr 370	GCC Ala	CTC Leu	CGG Arg	GTT Val	AAG Lys	AAC Asn 375	AAG Lys	CCC Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	GAG Glu	1691				
AAT Asn 385	GAA Glu	ATT Ile	CCC Pro	ACT Thr	CAT His 390	GTT Val	TTG Leu	CCA Pro	CCG Pro	TGT Cys 395	GCA Ala	AAT Asn	TTA Leu	CAG Gln	GCA Ala 400	1739				
CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGC Gly	AAT Asn 410	ACA Thr	CAC His	CTC Leu	TGT Cys	ATT Ile 415	TCC Ser	1787				
AAT Asn	GGT Gly	AAT Asn	TAT Tyr 420	GAA Glu	AAA Lys	GAA Glu	GGT Gly	CTC Leu 425	GGT Gly	GCT Ala	TCC Ser	AGC Ser	CAC His 430	ATA Ile	ACC Thr	1835				
ACA Thr	AAA Lys	TCA Ser 435	ATG Met	GCT Ala	GCT Ala	CCT Pro	CCA Pro 440	AGC Ser	TGT Cys	GGT Gly	CTG Leu	AGC Ser 445	CCA Pro	CTG Leu	CTG Leu	1883				
GTC Val	CTG Leu 450	GTG Val	GTA Val	ACC Thr	GCT Ala	CTG Leu 455	TCC Ser	ACC Thr	CTA Leu	TTA Leu	TCT Ser 460	TTA Leu	ACA Thr	GAA Glu	ACA Thr	1931				
TCA Ser 465	TAG *	CTGCATTAAA				AAAATACAAT		ATGGACATGT			AAAAAGACAA		AAACCAAGTT			1987				
ATCTGTTTCC TGTTCCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG TTGAGAAACA																2047				
GTTCCATTCA ACTGGAACAT TTTTTTTTTT NCCTTTTAAG AAAGCTTCTT GTGATCCTTC																2107				
GGGGCTTCTG TGAAAAACCT GATGCAGTGC TCCATCCAAA CTCAGAAGGC TTTGGGATAT																2167				
GCTGTATTTT AAAGGGACAG TTTGTAAC TT GGGCTGTAAA GCAAAC TGGG GCTGTGTTTT																2227				
CGATGATGAT GATCATCATG ATCATGATNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN																2287				
NNNNNNNGAT TTTAACAGTT TTA CTCTCTGG CCTTTCCTAG CTAGAGAAGG AGTTAATATT																2347				
TCTAAGGTAA CTCCCATATC TCCTTTAATG ACATTGATTT CTAATGATAT AAATTT CAGC																2407				

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CTACATTGAT GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG      2467
GAAACAGCTG GTACTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT      2527
TATGTACTGT AAACAGTTCT GCACTCTTGT AAAAAAGAAA AAACACCTGT CACATCCAAA      2587
TATAGTATCT GTCTTTTCGT CAAAATAGAG AGTGGGGAAT GAGTGTGCCG ATTCAATACC      2647
TCAATCCCTG AACGACACTC TCCTAATCCT AAGCCTTACC TGAGTGAGAA GCCCTTTACC      2707
TAACAAAAGT CCAATATAGC TGAAATGTCG CTCTAATACT CTTTACACAT ATGAGGTTAT      2767
ATGTAGAAAA AAATTTTACT ACTAAATGAT TTCAACTATT GGCTTTCTAT ATTTTGAAAG      2827
TAATGATATT GTCTCATTTT TTTACTGATG GTTTAATACA AAATACACAG AGCTTGTTTC      2887
CCCTCATAAG TAGTGTTTCG TCTGATATGA ACTTCACAAA TACAGCTCAT CAAAAGCAGA      2947
CTCTGAGAAG CCTCGTGCTG TAGCAGAAAG TTCTGCATCA TGTGACTGTG GACAGGCAGG      3007
AGGAAACAGA ACAGACAAGC ATTGTCTTTT GTCATTGCTC GAAGTGCAAG CGTGCATACC      3067
TGTGGAGGGA ACTGGTGGCT GCTTGTAAT GTTCTGCAGC ATCTCTTGAC ACACTTGTC      3127
TGACACAATC CAGTACCTTG GTTTTCAGGT TATCTGACAA AGGCAGCTTT GATTGGGACA      3187
TGGAGGCATG GGCAGGCCGG AA                                          3209

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1             5             10             15
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20             25             30
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35             40             45
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50             55             60
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65             70             75             80
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85             90             95
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100            105            110
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115            120            125

```

[illegible]

465

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..508
- (D) OTHER INFORMATION: /note= "1 to 508 is -237 to 272 of Figure 5 Hsgr-21af"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCACTAAC ATCCCTAACG	60
AGCATCCGAG CCGAGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT	120
CTCGAAGATT ACCGCATCTA TTTTTTTTTT CTTTTTTTTT TTTTCCTAGC GCAGATAAAG	180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTCG CCTGAAAGAA TAAATAAGTA	240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTCG GTTGAGTCCA GGTGGGGTCG	300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC	360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCCTCTTTC ACTGGATGGA GCTGAAC TTT	420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA	480
CCCAGCGGCG GCTCGGGATT TTTTGGG	508

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: /note= "1 to 510 is -237 to 272 of Figure 5 Hsgr-21bf"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA	60
CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG	120


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CTCTCGAAGA TTACCGCATC TATTTTTTTTTT TTCTTTTTTTT TCTTTTCCTA GCGCAGATAA      180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG      240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT      300
CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCC GCCCTC GCCATCCCGG AGCTGAGTCG      360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT      420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA      480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG      510

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1927 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 538..1926

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..537

(D) OTHER INFORMATION: /note= "1 to 537 is -235 to 301 of Figure 5 21acon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCACTAAC ATCCCTAACG      60
AGCATCCGAG CCGAGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT      120
CTCGAAGATT ACCGCATCTA TTTTTTTTTT CTTTTTTTTT TTTTCCTAGC GCAGATAAAG      180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTCG CCTGAAAGAA TAAATAAGTA      240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTCG GTTGAGTCCA GGTTGGGTCTG      300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC      360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCCTCTTTC ACTGGATGGA GCTGAACTTT      420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA      480
CCCAGCGGCG GCTCGGGATT TTTTTGGGGG GGCGGGGACC AGCCCCGCGC CGGCACC      537
ATG TTC CTG GCG NCC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC      585
Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
  1           5           10           15
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC      633
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
          20           25           30

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AGT Ser	GAT Asp	CAG Gln 35	TGC Cys	CTG Leu	AAG Lys	GAG Glu	CAG Gln 40	AGC Ser	TGC Cys	AGC Ser	ACC Thr	AAG Lys 45	TAC Tyr	CGC Arg	ACG Thr	681
CTA Leu	AGG Arg 50	CAG Gln	TGC Cys	GTG Val	GCG Ala	GGC Gly 55	AAG Lys	GAG Glu	ACC Thr	AAC Asn	TTC Phe 60	AGC Ser	CTG Leu	GCA Ala	TCC Ser	729
GGC Gly 65	CTG Leu	GAG Glu	GCC Ala	AAG Lys	GAT Asp 70	GAG Glu	TGC Cys	CGC Arg	AGC Ser	GCC Ala 75	ATG Met	GAG Glu	GCC Ala	CTG Leu	AAG Lys 80	777
CAG Gln	AAG Lys	TCG Ser	CTC Leu	TAC Tyr 85	AAC Asn	TGC Cys	CGC Arg	TGC Cys	AAG Lys 90	CGG Arg	GGT Gly	ATG Met	AAG Lys 95	AAG Lys 95	GAG Glu	825
AAG Lys	AAC Asn	TGC Cys	CTG Leu 100	CGC Arg	ATT Ile	TAC Tyr	TGG Trp	AGC Ser 105	ATG Met	TAC Tyr	CAG Gln	AGC Ser	CTG Leu 110	CAG Gln	GGA Gly	873
AAT Asn	GAT Asp 115	CTG Leu	CTG Leu	GAG Glu	GAT Asp	TCC Ser	CCA Pro 120	TAT Tyr	GAA Glu	CCA Pro	GTT Val	AAC Asn 125	AGC Ser	AGA Arg	TTG Leu	921
TCA Ser 130	GAT Asp	ATA Ile	TTC Phe	CGG Arg	GTG Val	GTC Val 135	CCA Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTT Phe	CAG Gln	CAA Gln	969
GTG Val 145	GAG Glu	CAC His	ATT Ile	CCC Pro	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAT Asp	GCA Ala	GCG Ala	AAG Lys	GCC Ala 160	1017
TGC Cys	AAC Asn	CTC Leu	GAC Asp	GAC Asp 165	ATT Ile	TGC Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCG Ala	TAC Tyr	ATC Ile 175	ACC Thr	1065
CCG Pro	TGC Cys	ACC Thr 180	ACC Thr	AGC Ser	GTG Val	TCC Ser	AAC Asn	GAT Asp 185	GTC Val	TGC Cys	AAC Asn	CGC Arg 190	CGC Arg	AAG Lys	TGC Cys	1113
CAC His	AAG Lys 195	GCC Ala	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1161
TAC Tyr 210	GGA Gly	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1209
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1257
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC Ile 255	TGC Cys	1305
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe 265	ACC Thr	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1353
TCT Ser	GTC Val	AGC Ser 275	AGC Ser	TGT Cys	CTA Leu	AAG Lys	GAA Glu 280	AAC Asn	TAC Tyr	GCT Ala	GAC Asp	TGC Cys 285	CTC Leu	CTC Leu	GCC Ala	1401

TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	CCC	AAC	TAC	ATA	GAC	TCC	1449
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	
	290					295					300					
AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	TGC	AGC	AAC	AGT	GGG	AAC	1497
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
305					310					315					320	
GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	TTC	TTC	AAG	GAC	AAT	ACA	1545
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
				325					330					335		
TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	AAT	GGC	TCC	GAT	GTG	ACC	1593
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
			340					345					350			
GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	ACC	ACT	GCC	ACT	ACC	ACC	1641
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	
		355					360					365				
ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	GGG	CCA	GCA	GGG	TCT	GAG	1689
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	
	370					375					380					
AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	TGT	GCA	AAT	TTA	CAG	GCA	1737
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	
385					390					395					400	
CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGC	AAT	ACA	CAC	CTC	TGT	ATT	TCC	1785
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser	
				405					410					415		
AAT	GGT	AAT	TAT	GAA	AAA	GAA	GGT	CTC	GGT	GCT	TCC	AGC	CAC	ATA	ACC	1833
Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr	
			420				425						430			
ACA	AAA	TCA	ATG	GCT	GCT	CCT	CCA	AGC	TGT	GGT	CTG	AGC	CCA	CTG	CTG	1881
Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Gly	Leu	Ser	Pro	Leu	Leu	
		435					440					445				
GTC	CTG	GTG	GTA	ACC	GCT	CTG	TCC	ACC	CTA	TTA	TCT	TTA	ACA	GAA		1926
Val	Leu	Val	Val	Thr	Ala	Leu	Ser	Thr	Leu	Leu	Ser	Leu	Thr	Glu		
	450					455					460					
A																1927

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30

Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr
		35					40					45			
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Ala	Ser
	50					55					60				
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys
65					70					75					80
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu
				85					90					95	
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly
			100					105					110		
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu
		115					120					125			
Ser	Asp	Ile	Phe	Arg	Val	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln
	130					135					140				
Val	Glu	His	Ile	Pro	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala
145					150					155					160
Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr
				165					170					175	
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys
			180					185					190		
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser
		195					200					205			
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg
	210					215					220				
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys
225					230					235					240
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys
				245					250					255	
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg
			260					265					270		
Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala
		275					280					285			
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser
	290					295					300				
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn
305					310					315					320
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr
				325					330					335	
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr
			340					345					350		
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr
		355					360					365			
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu

370		375		380
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala				
385		390		395 400
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser				
	405		410	415
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr				
	420		425	430
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu				
	435		440	445
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu				
450		455		460

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1929 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 540..1928

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of

Figure 5 21bcon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA	60
CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG	120
CTCTCGAAGA TTACCGCATC TATTTTTTTT TTCTTTTTTT TCTTTTCCTA GCGCAGATAA	180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG	240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT	300
CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCCGCCCTC GCCATCCCGG AGCTGAGTCG	360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT	420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA	480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG GGGGCGGGGA CCAGCCCCGC GCCGGCACC	539
ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC	587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu	
1 5 10 15	
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC	635

Leu	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala	
			20					25					30			
AGT	GAT	CAG	TGC	CTG	AAG	GAG	CAG	AGC	TGC	AGC	ACC	AAG	TAC	CGC	ACG	683
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	
		35					40					45				
CTA	AGG	CAG	TGC	GTG	GCG	GGC	AAG	GAG	ACC	AAC	TTC	AGC	CTG	GCA	TCC	731
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Ala	Ser	
	50					55					60					
GGC	CTG	GAG	GCC	AAG	GAT	GAG	TGC	CGC	AGC	GCC	ATG	GAG	GCC	CTG	AAG	779
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys	
65				70						75					80	
CAG	AAG	TCG	CTC	TAC	AAC	TGC	CGC	TGC	AAG	CGG	GGT	ATG	AAG	AAG	GAG	827
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	
				85					90					95		
AAG	AAC	TGC	CTG	CGC	ATT	TAC	TGG	AGC	ATG	TAC	CAG	AGC	CTG	CAG	GGA	875
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly	
			100					105					110			
AAT	GAT	CTG	CTG	GAG	GAT	TCC	CCA	TAT	GAA	CCA	GTT	AAC	AGC	AGA	TTG	923
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu	
		115					120					125				
TCA	GAT	ATA	TTC	CGG	GTG	GTC	CCA	TTC	ATA	TCA	GAT	GTT	TTT	CAG	CAA	971
Ser	Asp	Ile	Phe	Arg	Val	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln	
	130					135					140					
GTG	GAG	CAC	ATT	CCC	AAA	GGG	AAC	AAC	TGC	CTG	GAT	GCA	GCG	AAG	GCC	1019
Val	Glu	His	Ile	Pro	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	
145				150						155					160	
TGC	AAC	CTC	GAC	GAC	ATT	TGC	AAG	AAG	TAC	AGG	TCG	GCG	TAC	ATC	ACC	1067
Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	
				165					170					175		
CCG	TGC	ACC	ACC	AGC	GTG	TCC	AAC	GAT	GTC	TGC	AAC	CGC	CGC	AAG	TGC	1115
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	
			180					185					190			
CAC	AAG	GCC	CTC	CGG	CAG	TTC	TTT	GAC	AAG	GTC	CCG	GCC	AAG	CAC	AGC	1163
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	
		195					200					205				
TAC	GGA	ATG	CTC	TTC	TGC	TCC	TGC	CGG	GAC	ATC	GCC	TGC	ACA	GAG	CGG	1211
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	
	210					215					220					
AGG	CGA	CAG	ACC	ATC	GTG	CCT	GTG	TGC	TCC	TAT	GAA	GAG	AGG	GAG	AAG	1259
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys	
225				230						235					240	
CCC	AAC	TGT	TTG	AAT	TTG	CAG	GAC	TCC	TGC	AAG	ACG	AAT	TAC	ATC	TGC	1307
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	
				245					250					255		
AGA	TCT	CGC	CTT	GCG	GAT	TTT	TTT	ACC	AAC	TGC	CAG	CCA	GAG	TCA	AGG	1355
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg	
			260					265					270			
TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	GCT	GAC	TGC	CTC	CTC	GCC	1403

Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	
		275					280					285				
TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	CCC	AAC	TAC	ATA	GAC	TCC	1451
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	
	290					295					300					
AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	TGC	AGC	AAC	AGT	GGG	AAC	1499
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
305					310					315					320	
GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	TTC	TTC	AAG	GAC	AAT	ACA	1547
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
				325					330					335		
TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	AAT	GGC	TCC	GAT	GTG	ACC	1595
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
			340					345					350			
GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	ACC	ACT	GCC	ACT	ACC	ACC	1643
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	
		355					360					365				
ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	GGG	CCA	GCA	GGG	TCT	GAG	1691
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	
	370					375					380					
AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	TGT	GCA	AAT	TTA	CAG	GCA	1739
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	
385					390					395					400	
CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGC	AAT	ACA	CAC	CTC	TGT	ATT	TCC	1787
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser	
				405					410					415		
AAT	GGT	AAT	TAT	GAA	AAA	GAA	GGT	CTC	GGT	GCT	TCC	AGC	CAC	ATA	ACC	1835
Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr	
			420				425						430			
ACA	AAA	TCA	ATG	GCT	GCT	CCT	CCA	AGC	TGT	GGT	CTG	AGC	CCA	CTG	CTG	1883
Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Gly	Leu	Ser	Pro	Leu	Leu	
		435					440					445				
GTC	CTG	GTG	GTA	ACC	GCT	CTG	TCC	ACC	CTA	TTA	TCT	TTA	ACA	GAA		1928
Val	Leu	Val	Val	Thr	Ala	Leu	Ser	Thr	Leu	Leu	Ser	Leu	Thr	Glu		
	450					455					460					
A																1929

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe	Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu	
1				5					10					15		
M	V	L	A	T	L	Y	F	A	L	P	L	L	N	L	L	

Leu	Ser	Ala	Glu	Val	Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala	
			20					25					30			
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	
		35					40					45				
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Ala	Ser	
	50					55					60					
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys	
65					70					75					80	
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	
				85					90					95		
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly	
			100					105					110			
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu	
		115					120					125				
Ser	Asp	Ile	Phe	Arg	Val	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln	
	130					135					140					
Val	Glu	His	Ile	Pro	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	
145					150					155					160	
Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	
				165					170					175		
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	
			180					185					190			
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	
		195					200					205				
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	
	210					215					220					
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys	
225					230					235					240	
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	
				245					250					255		
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg	
			260					265					270			
Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	
		275					280					285				
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	
	290					295					300					
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
305					310					315					320	
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
				325					330					335		
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
			340					345					350			
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	

355	360	365
Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu		
370	375	380
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala		
385	390	395
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser		
	405	410
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr		
	420	425
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu		
	435	440
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu		
	450	455
		460

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..699
- (D) OTHER INFORMATION: /note= "1 to 699 is 814 to 1512 of

Figure 5 Hsgr-29a"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

G TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC AAT GAT GTC	46
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val	
1 5 10 15	
TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG	94
Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys	
20 25 30	
GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC	142
Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp	
35 40 45	
ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC	190
Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser	
50 55 60	
TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC	238
Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys	
65 70 75	

AAG	ACG	AAT	TAC	ATC	TGC	AGA	TCT	CGC	CTT	GCG	GAT	TTT	TTT	ACC	AAC	286
Lys	Thr	Asn	Tyr	Ile	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	
80					85					90					95	
TGC	CAG	CCA	GAG	TCA	AGG	TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	334
Cys	Gln	Pro	Glu	Ser	Arg	Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	
				100					105					110		
GCT	GAC	TGC	CTC	CTC	GCC	TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	382
Ala	Asp	Cys	Leu	Leu	Ala	Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	
			115					120					125			
CCC	AAC	TAC	ATA	GAC	TCC	AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	430
Pro	Asn	Tyr	Ile	Asp	Ser	Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	
		130					135					140				
TGC	AGC	AAC	AGT	GGG	AAC	GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	478
Cys	Ser	Asn	Ser	Gly	Asn	Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	
	145					150					155					
TTC	TTC	AAG	GAC	AAT	ACA	TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	526
Phe	Phe	Lys	Asp	Asn	Thr	Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	
160					165					170					175	
AAT	GGC	TCC	GAT	GTG	ACC	GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	574
Asn	Gly	Ser	Asp	Val	Thr	Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	
				180					185					190		
ACC	ACT	GCC	GCT	ACC	ACC	ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	622
Thr	Thr	Ala	Ala	Thr	Thr	Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	
			195					200					205			
GGG	CCA	GCA	GGG	TCT	GAG	AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	670
Gly	Pro	Ala	Gly	Ser	Glu	Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	
		210					215					220				
TGT	GCA	AAT	TTA	CAG	GCA	CAG	AAG	CTG	AA							699
Cys	Ala	Asn	Leu	Gln	Ala	Gln	Lys	Leu								
	225					230										

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser	Ala	Tyr	Ile	Thr	Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys
1				5					10					15	
Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val
			20					25					30		
Pro	Ala	Lys	His	Ser	Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile
		35					40					45			
Ala	Cys	Thr	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr
	50					55					60				

Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
 65 70 75 80
 Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 85 90 95
 Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
 100 105 110
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
 115 120 125
 Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
 130 135 140
 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
 145 150 155 160
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
 165 170 175
 Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
 180 185 190
 Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
 195 200 205
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
 210 215 220
 Ala Asn Leu Gln Ala Gln Lys Leu
 225 230

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..886

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..2157
- (D) OTHER INFORMATION: /note= "1 to 2157 is 814 to 2971 of

Figure 5 29brc"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

G	TCG	GCG	TAC	ATC	ACC	CCG	TGC	ACC	ACC	AGC	GTG	TCC	AAT	GAT	GTC	46
Ser	Ala	Tyr	Ile	Thr	Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val		
1				5					10					15		
TGC	AAC	CGC	CGC	AAG	TGC	CAC	AAG	GCC	CTC	CGG	CAG	TTC	TTT	GAC	AAG	94
Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	
				20					25					30		

GTC	CCG	GCC	AAG	CAC	AGC	TAC	GGA	ATG	CTC	TTC	TGC	TCC	TGC	CGG	GAC	142
Val	Pro	Ala	Lys	His	Ser	Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	
			35					40					45			
ATC	GCC	TGC	ACA	GAG	CGG	AGG	CGA	CAG	ACC	ATC	GTG	CCT	GTG	TGC	TCC	190
Ile	Ala	Cys	Thr	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	
		50					55					60				
TAT	GAA	GAG	AGG	GAG	AAG	CCC	AAC	TGT	TTG	AAT	TTG	CAG	GAC	TCC	TGC	238
Tyr	Glu	Glu	Arg	Glu	Lys	Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	
	65					70					75					
AAG	ACG	AAT	TAC	ATC	TGC	AGA	TCT	CGC	CTT	GCG	GAT	TTT	TTT	ACC	AAC	286
Lys	Thr	Asn	Tyr	Ile	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	
80					85					90					95	
TGC	CAG	CCA	GAG	TCA	AGG	TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	334
Cys	Gln	Pro	Glu	Ser	Arg	Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	
				100				105						110		
GCT	GAC	TGC	CTC	CTC	GCC	TAC	TCG	GGG	CTT	ATT	GGC	ACA	GTC	ATG	ACC	382
Ala	Asp	Cys	Leu	Leu	Ala	Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	
			115					120					125			
CCC	AAC	TAC	ATA	GAC	TCC	AGT	AGC	CTC	AGT	GTG	GCC	CCA	TGG	TGT	GAC	430
Pro	Asn	Tyr	Ile	Asp	Ser	Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	
		130					135					140				
TGC	AGC	AAC	AGT	GGG	AAC	GAC	CTA	GAA	GAG	TGC	TTG	AAA	TTT	TTG	AAT	478
Cys	Ser	Asn	Ser	Gly	Asn	Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	
	145					150					155					
TTC	TTC	AAG	GAC	AAT	ACA	TGT	CTT	AAA	AAT	GCA	ATT	CAA	GCC	TTT	GGC	526
Phe	Phe	Lys	Asp	Asn	Thr	Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	
160					165					170					175	
AAT	GGC	TCC	GAT	GTG	ACC	GTG	TGG	CAG	CCA	GCC	TTC	CCA	GTA	CAG	ACC	574
Asn	Gly	Ser	Asp	Val	Thr	Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	
				180					185					190		
ACC	ACT	GCC	GCT	ACC	ACC	ACT	GCC	CTC	CGG	GTT	AAG	AAC	AAG	CCC	CTG	622
Thr	Thr	Ala	Ala	Thr	Thr	Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	
			195					200					205			
GGG	CCA	GCA	GGG	TCT	GAG	AAT	GAA	ATT	CCC	ACT	CAT	GTT	TTG	CCA	CCG	670
Gly	Pro	Ala	Gly	Ser	Glu	Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	
		210					215					220				
TGT	GCA	AAT	TTA	CAG	GCA	CAG	AAG	CTG	AAA	TCC	AAT	GTG	TCG	GGC	AAT	718
Cys	Ala	Asn	Leu	Gln	Ala	Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	
	225					230					235					
ACA	CAC	CTC	TGT	ATT	TCC	AAT	GGT	AAT	TAT	GAA	AAA	GAA	GGT	CTC	GGT	766
Thr	His	Leu	Cys	Ile	Ser	Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	
240					245					250					255	
GCT	TCC	AGC	CAC	ATA	ACC	ACA	AAA	TCA	ATG	GCT	GCT	CCT	CCA	AGC	TGT	814
Ala	Ser	Ser	His	Ile	Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	
				260					265					270		
GGT	CTG	AGC	CCA	CTG	CTG	GTC	CTG	GTG	GTA	ACC	GCT	CTG	TCC	ACC	CTA	862
Gly	Leu	Ser	Pro	Leu	Leu	Val	Leu	Val	Val	Thr	Ala	Leu	Ser	Thr	Leu	
			275					280					285			

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TTA TCT TTA ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT      916
Leu Ser Leu Thr Glu Thr Ser *
      290                      295

AAAAAGACAA AAACCAAGTT ATCTGTTTCC TGTTCCTCTTG TATAGCTGAA ATTCCAGTTT      976
AGGAGCTCAG TTGAGAAACA GTTCCATTCA ACTGGAACAT TTTTTTTTTT CCTTTTAAGA      1036
AAGCTTCTTG TGATCCTTCG GGGCTTCTGT GAAAAACCTG ATGCAGTGCT CCATCCAAAC      1096
TCAGAAGGCT TTGGGATATG CTGTATTTTA AAGGGACAGT TTGTAACCTG GGCTGTAAAG      1156
CAAACCTGGGG CTGTGTTTTTC GATGATGATG ATCATCATGA TCATGATNNN NNNNNNNNNN      1216
NNNNNNNNNN NNNNNNNNNN NNNNNNGATT TTAACAGTTT TACTTCTGGC CTTTCCTAGC      1276
TAGAGAAGGA GTTAATATTT CTAAGGTAAC TCCCATATCT CCTTTAATGA CATTGATTTT      1336
TAATGATATA AATTTTCAGCC TACATTGATG CCAAGCTTTT TTGCCACAAA GAAGATTCTT      1396
ACCAAGAGTG GGCTTTGTGG AAACAGCTGG TACTGATGTT CACCTTTATA TATGTACTAG      1456
CATTTTCCAC GCTGATGTTT ATGTACTGTA AACAGTTCTG CACTCTTGTA CAAAAGAAAA      1516
AACACCTGTC ACATCCAAAT ATAGTATCTG TCTTTTCGTC AAAATAGAGA GTGGGGAATG      1576
AGTGTGCCGA TTCAATACCT CAATCCCTGA ACGACACTCT CCTAATCCTA AGCCTTACCT      1636
GAGTGAGAAG CCCTTTACCT AACAAAAGTC CAATATAGCT GAAATGTCGC TCTAATACTC      1696
TTTACACATA TGAGGTTATA TGTAGAAAAA AATTTTACTA CTAAATGATT TCAACTATTG      1756
GCTTTCTATA TTTTGAAAGT AATGATATTG TCTCATTTTT TTAAGTATGG TTTAATACAA      1816
AATACACAGA GCTTGTTTCC CCTCATAAGT AGTGTTTCGCT CTGATATGAA CTTACAAAT      1876
ACAGCTCATC AAAAGCAGAC TCTGAGAAGC CTCGTGCTGT AGCAGAAAGT TCTGCATCAT      1936
GTGACTGTGG ACAGGCAGGA GGAAACAGAA CAGACAAGCA TTGTCTTTTG TCATTGCTCG      1996
AAGTGCAAGC GTGCATACCT GTGGAGGGAA CTGGTGCTGT CTTGTAAATG TTCTGCAGCA      2056
TCTCTTGACA CACTTGTCAT GACACAATCC AGTACCTTGG TTTTCAGGTT ATCTGACAAA      2116
GGCAGCTTTG ATTGGGACAT GGAGGCATGG GCAGGCCGGA A                          2157

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(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
 1           5           10           15
Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
      20           25           30

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Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
 35 40 45
 Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
 50 55 60
 Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
 65 70 75 80
 Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 85 90 95
 Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
 100 105 110
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
 115 120 125
 Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
 130 135 140
 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
 145 150 155 160
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
 165 170 175
 Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
 180 185 190
 Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
 195 200 205
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
 210 215 220
 Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr
 225 230 235 240
 His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala
 245 250 255
 Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly
 260 265 270
 Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu
 275 280 285
 Ser Leu Thr Glu Thr Ser *
 290 295

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..658

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..659
(D) OTHER INFORMATION: /note= "1 to 659 is 1033 to 1691 of
Figure 5 Hsgr-21ar"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

G AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC	46
Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg	
1 5 10 15	
CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG TCT GTC AGC	94
Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser	
20 25 30	
AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC TAC TCG GGG	142
Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly	
35 40 45	
CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC AGT AGC CTC	190
Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu	
50 55 60	
AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC GAC CTA GAA	238
Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu	
65 70 75	
GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA	286
Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys	
80 85 90 95	
AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG	334
Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln	
100 105 110	
CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC	382
Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu	
115 120 125	
CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT	430
Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile	
130 135 140	
CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG	478
Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu	
145 150 155	
AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT	526
Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn	
160 165 170 175	
TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA	574
Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser	
180 185 190	
ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG	622
Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val	
195 200 205	

GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA A
 Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 210 215

659

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu
 1 5 10 15
 Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser
 20 25 30
 Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu
 35 40 45
 Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser
 50 55 60
 Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu
 65 70 75 80
 Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
 85 90 95
 Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
 100 105 110
 Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
 115 120 125
 Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
 130 135 140
 Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
 145 150 155 160
 Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
 165 170 175
 Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
 180 185 190
 Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
 195 200 205
 Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 210 215

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..630

(D) OTHER INFORMATION: /note= "1 to 630 is 1062 to 1691 of Figure 5 Hsgr-21br"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AC ATC TGC AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA	47
Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro	
1 5 10 15	
GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC	95
Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys	
20 25 30	
CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC	143
Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr	
35 40 45	
ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC	191
Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn	
50 55 60	
AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG	239
Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys	
65 70 75	
GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC	287
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser	
80 85 90 95	
GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC	335
Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala	
100 105 110	
ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA	383
Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala	
115 120 125	
GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT	431
Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn	
130 135 140	
TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC	479
Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu	
145 150 155	
TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC	527
Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser	
160 165 170 175	
CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC	575
His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser	

[illegible]

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

[illegible]

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..445

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1075

(D) OTHER INFORMATION: /note= "1 to 1075 is 1255 to 2330
of Figure 5 Hsgr-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

T GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG	46
Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys	
1 5 10 15	
GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC	94
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser	
20 25 30	
GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC	142
Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala	
35 40 45	
ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA	190
Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala	
50 55 60	
GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT	238
Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn	
65 70 75	
TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC	286
Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu	
80 85 90 95	
TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC	334
Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser	
100 105 110	
CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC	382
His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser	
115 120 125	
CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA	430
Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu	
130 135 140	
ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA	485
Thr Glu Thr Ser *	
145	

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AAACCAAGTT ATCTGTTTCC TGTTCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG      545
TTGAGAAAACA GTTCCATTCA ACTGGAACAT TTTT TTTT TTTT CCTTTTAAGA AAGCTTCTTG      605
TGATCCTTCG GGGCTTCTGT GAAAAACCTG ATGCAGTGCT CCATCCAAAC TCAGAAGGCT      665
TTGGGATATG CTGTATTTTA AAGGGACAGT TTGTAAGTTG GGCTGTAAAG CAAACTGGGG      725
CTGTGTTTTTC GATGATGATG ATCATCATGA TCATGATNNN NNNNNNNNNN NNNNNNNNNN      785
NNNNNNNNNN NNNNNNGATT TTAACAGTTT TACTTCTGGC CTTTCCTAGC TAGAGAAGGA      845
GTTAATATTT CTAAGGTAAC TCCCATATCT CCTTTAATGA CATTGATTTC TAATGATATA      905
AATTCAGCC TACATTGATG CCAAGCTTTT TTGCCACAAA GAAGATTCTT ACCAAGAGTG      965
GGCTTTGTGG AAACAGCTGG TACTGATGTT CACCTTTATA TATGTACTAG CATTTTCCAC     1025
GCTGATGTTT ATGTACTGTA AACAGTTCTG CACTCTTGTA CAAAAGAAAA     1075

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
 1          5          10          15
Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
          20          25          30
Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
          35          40          45
Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
          50          55          60
Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
          65          70          75          80
Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
          85          90          95
Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
          100          105          110
Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
          115          120          125
Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
          130          135          140
Glu Thr Ser *
145

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..428

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1059
- (D) OTHER INFORMATION: /note= "1 to 1059 is 1272 to 2330

of Figure 5 Hsgr-9"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA	47
Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys	
1 5 10 15	
AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG	95
Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln	
20 25 30	
CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC	143
Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu	
35 40 45	
CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT	191
Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile	
50 55 60	
CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG	239
Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu	
65 70 75	
AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT	287
Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn	
80 85 90 95	
TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA	335
Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser	
100 105 110	
ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG	383
Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val	
115 120 125	
GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA TCA TAG	428
Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser *	
130 135 140	
CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA AAACCAAGTT ATCTGTTTCC	488
TGTTCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG TTGAGAAACA GTTCCATTCA	548
ACTGGAACAT TTTTTTTTTT TCCTTTTAAG AAAGCTTCTT GTGATCCTTT GGGGCTTCTG	608

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TGAAAAACCT GATGCAGTGC TCCATCCAAA CTCAGAAGGC TTTGGGATAT GCTGTATTTT      668
AAAGGGACAG TTTGTAACTT GGGCTGTAAA GCAAAGTGGG GCTGTGTTTT CGATGATGAT      728
GATGATCATG ATGATGATCA TCATGATCAT GATGATGATC ATCATGATCA TGATGATGAT      788
TTTAACAGTT TTAATTCTGG CCTTTCCTAG CTAGAGAAGG AGTTAATATT TCTAAGGTAA      848
CTCCCATATC TCCTTTAATG ACATTGATTT CTAATGATAT AAATTTTCAGC CTACATTGAT      908
GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG GAAACAGCTG      968
GTACTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT TATGTACTGT     1028
AAACAGTTCT GCACTCTTGT ACAAAGAAA A                                     1059

```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
 1           5           10
Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
          20           25           30
Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
          35           40           45
Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
          50           55           60
Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
          65           70           75           80
Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
          85           90           95
Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
          100          105          110
Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
          115          120          125
Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser *
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr	Leu
1				5					10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Lys	Asn
1				5					10

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val
1				5					10

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg	Pro	Asn
1				5					10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Pro	Ala	Pro	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	Thr
1				5					10				

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGTTTGAAT TTGCAGGACT C

21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTCCTCTCTA AGCTTCTAAC CACAGCTTGG AGGAGC

36

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
CTCCTCTCTA AGCTTCTATG GGCTCAGACC ACAGCTT 37

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCACCACAGC TTGGAGGAGC 60

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCTGGCTCAG ACCACAGCTT 60

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1587..2978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
CATGAAGAAA CCTCAGTAAG TCTCAGACTT GGCCCAAAGG AGCCCAACTA GTTACTCCCT 60
GGTCTGTTAC AGAGGATCTG GCTATTACAC TCAACAGCAA AAATTCAATT CAATCCCGCT 120
AAAGATATAA GAATCACTAG GAAKAATAAG CCAGAACTCA AGACAGAAAT AGCATTAAGT 180

AGTTCCTTCA	GTACAGTGAG	CAGAAGCTGG	CCACTCTACG	ACTCTAWAAG	ACTCAGAAAA	240
GCTTACTAGG	GACCWCTGGG	CATWCCGGTG	TCCTATGTGG	GGATTTCGTA	ACGTCTTTGA	300
GTCAGAAAGCT	GCCCTCAAAA	TAGTTTCTTC	TCAAAACGGT	TTCAGGCTTT	GTTAGAAAGG	360
GAAGACTTCA	CTGCCACTTT	ACCCAGATCA	TCTACCCCAT	CCTTGGAATG	AATGGGGAAG	420
CTTCAGCCAC	CCTACCAGGC	TCCTAAAATC	ACCAACTTGA	GAGAAAAACT	ATAACGTTCG	480
TCTACCAGTA	CTTCAGGAGG	TTAAAGAAAG	TCACAGAAAG	AAAGAACTCT	GGGGAAAACA	540
GTCAAATTCG	GCTATTAAGA	CATTAGTTAC	AGGCCCCCTGT	ACCTCTCCTC	TAGAAACCCCT	600
GGGAGTACAC	CCGCAGAGGA	GAGAGAGCCC	AAGCCACCAA	GCAAAGTCAA	CCAATCTGGC	660
AAAGGGGCGT	CCCACTGCGG	CTTTCAGTCC	AAGAAGTGGA	TCCTGCTGGT	TCGCAGTCTC	720
TCTTCTATCT	CCTCACTTCC	TATTTACCCCT	TTGAAGTGGG	TACTGAATAG	CCCGTTCCCA	780
AGCAGAGGCC	CTTTGTATAC	GGGGTGCTAC	AGTCGCCTGG	TGGAAACACC	TTGGCAGAGT	840
TGTTTGGTGC	CAGGATGGGC	CACTGAAGGC	ATCTGCTGTG	GACACACACA	CACACACACA	900
CACACACACA	CACACACACA	GAGAGAGGAG	AGAGAAAAGAC	ACACGCACGC	AGAGACACAC	960
GGTCACTGGA	ATTCCATTAG	AAAAAAGTGA	GCCGAGCAAG	GGTTAGCGGG	AGAAGATTTT	1020
TTTGAATCTT	GTCTTCGTCT	TGGTGCGAAA	GAAGCGACTC	CAGTCTCTCG	TCCTCGAAGC	1080
TCCGACTGGA	TTGTTCTTGG	GCGCTGACAC	CCGTCTGTGG	ATTTCTTTTC	TATTTGCATT	1140
TTATTCCGAC	CCCCTCCCTC	GCCGCTTCCT	TCCAGCCCTT	CACTCGCAAA	TCGCCTCTCT	1200
CCCCACCTCC	CCAGGCCCTC	CCTGGGAAGC	GCAGGGGAAT	TGGACCCGCG	GGGACTCACG	1260
CCTTCCCGGA	CGATTGGAGG	GGAGGGCTGA	CCCCAGGACT	GGGCTGTTGG	CTTAGAAAGC	1320
CGATACACAG	ATACGCGTAT	ATTTGATTGT	AGCGGGCAAG	GGGGGCGTCG	AGAGGCAGCA	1380
GCCCATCGCC	CGCCTCTCAC	CCCACCCCTT	CCAGCCAGAG	GCGAGAATCG	CAGGACTCGG	1440
GATCTTCATC	GGGTGGACTA	GCTGGGATCT	CCGCATTGGA	TTTGGGGCTG	ATTACCACTG	1500
CTTGGCTATT	ATTATTGTTG	TTGTTACTAC	TATTATTTTTT	TTTTACCCAA	GGGAGAAAGA	1560
CAAAAAAACG	GTGGGATTTA	TTTAAC	ATG ATC TTG GCA AAC GTC TTC TGC CTC			1613
			Met Ile Leu Ala Asn Val Phe Cys Leu			
			1	5		
TTC TTC TTT CTA GAC GAC ACC CTC CGC TCT TTG GCC AGC CCT TCC TCC						1661
Phe Phe Phe Leu Asp Asp Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser						
10	15	20	25			
CTG CAG GGC CCC GAG CTC CAC GGC TGG CGC CCC CCA GTG GAC TGT GTC						1709
Leu Gln Gly Pro Glu Leu His Gly Trp Arg Pro Pro Val Asp Cys Val						
	30	35	40			
CGG GCC AAT GAG CTG TGT GCC GCC GAA TCC AAC TGC AGC TCT CGC TAC						1757
Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr						
	45	50	55			
CGC ACT CTG CGG CAG TGC CTG GCA GGC CGC GAC CGC AAC ACC ATG CTG						1805
Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu						

60					65					70						
GCC Ala	AAC Asn 75	AAG Lys	GAG Glu	TGC Cys	CAG Gln 80	GCG Ala	GCC Ala	TTG Leu	GAG Glu	GTC Val	TTG Leu 85	CAG Gln	GAG Glu	AGC Ser	CCG Pro	1853
CTG Leu 90	TAC Tyr	GAC Asp	TGC Cys	CGC Arg	TGC Cys 95	AAG Lys	CGG Arg	GGC Gly	ATG Met	AAG Lys 100	AAG Lys	GAG Glu	CTG Leu	CAG Gln	TGT Cys 105	1901
CTG Leu	CAG Gln	ATC Ile	TAC Tyr	TGG Trp 110	AGC Ser	ATC Ile	CAC His	CTG Leu	GGG Gly 115	CTG Leu	ACC Thr	GAG Glu	GGT Gly	GAG Glu 120	GAG Glu	1949
TTC Phe	TAC Tyr	GAA Glu 125	GCC Ala	TCC Ser	CCC Pro	TAT Tyr	GAG Glu	CCG Pro 130	GTG Val	ACC Thr	TCC Ser	CGC Arg	CTC Leu 135	TCG Ser	GAC Asp	1997
ATC Ile	TTC Phe	AGG Arg 140	CTT Leu	GCT Ala	TCA Ser	ATC Ile	TTC Phe 145	TCA Ser	GGG Gly	ACA Thr	GGG Gly	GCA Ala 150	GAC Asp	CCG Pro	GTG Val	2045
GTC Val	AGC Ser 155	GCC Ala	AAG Lys	AGC Ser	AAC Asn	CAT His 160	TGC Cys	CTG Leu	GAT Asp	GCT Ala	GCC Ala 165	AAG Lys	GCC Ala	TGC Cys	AAC Asn	2093
CTG Leu 170	AAT Asn	GAC Asp	AAC Asn	TGC Cys	AAG Lys 175	AAG Lys	CTG Leu	CGC Arg	TCC Ser	TCC Ser 180	TAC Tyr	ATC Ile	TCC Ser	ATC Ile	TGC Cys 185	2141
AAC Asn	CGC Arg	GAG Glu	ATC Ile	TCG Ser 190	CCC Pro	ACC Thr	GAG Glu	CGC Arg	TGC Cys 195	AAC Asn	CGC Arg	CGC Arg	AAG Lys	TGC Cys 200	CAC His	2189
AAG Lys	GCC Ala	CTG Leu	CGC Arg 205	CAG Gln	TTC Phe	TTC Phe	GAC Asp 210	CGG Arg	GTG Val	CCC Pro	AGC Ser	GAG Glu	TAC Tyr 215	ACC Thr	TAC Tyr	2237
CGC Arg	ATG Met	CTC Leu 220	TTC Phe	TGC Cys	TCC Ser	TGC Cys	CAA Gln 225	GAC Asp	CAG Gln	GCG Ala	TGC Cys	GCT Ala 230	GAG Glu	CGC Arg	CGC Arg	2285
CGG Arg	CAA Gln 235	ACC Thr	ATC Ile	CTG Leu	CCC Pro	AGC Ser 240	TGC Cys	TCC Ser	TAT Tyr	GAG Glu	GAC Asp 245	AAG Lys	GAG Glu	AAG Lys	CCC Pro	2333
AAC Asn 250	TGC Cys	CTG Leu	GAC Asp	CTG Leu	CGT Arg 255	GGC Gly	GTG Val	TGC Cys	CGG Arg	ACT Thr 260	GAC Asp	CAC His	CTG Leu	TGT Cys	CGG Arg 265	2381
TCC Ser	CGG Arg	CTG Leu	GCC Ala	GAC Asp 270	TTC Phe	CAT His	GCC Ala	AAT Asn	TGT Cys 275	CGA Arg	GCC Ala	TCC Ser	TAC Tyr	CAG Gln 280	ACG Thr	2429
GTC Val	ACC Thr	AGC Ser	TGC Cys 285	CCT Pro	GCG Ala	GAC Asp	AAT Asn	TAC Tyr 290	CAG Gln	GCG Ala	TGT Cys	CTG Leu	GGC Gly 295	TCT Ser	TAT Tyr	2477
GCT Ala	GGC Gly 300	ATG Met	ATT Ile	GGG Gly	TTT Phe	GAC Asp 305	ATG Met	ACA Thr	CCT Pro	AAC Asn	TAT Tyr 310	GTG Val	GAC Asp	TCC Ser	AGC Ser	2525
CCC Pro	ACT Thr	GGC Gly	ATC Ile	GTG Val	GTG Val	TCC Ser	CCC Pro	TGG Trp	TGC Cys	AGC Ser	TGT Cys	CGT Arg	GGC Gly	AGC Ser	GGG Gly	2573

315	320	325	
AAC ATG GAG GAG GAG TGT GAG AAG TTC CTC AGG GAC TTC ACC GAG AAC Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn 330 335 340 345			2621
CCA TGC CTC CGG AAC GCC ATC CAG GCC TTT GGC AAC GGC ACG AAC GTG Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asn Val 350 355 360			2669
AAC GTG TCC CCA AAA GGC CCC TCG TTC CAG GCC ACC CAG GCC CCT CGG Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg 365 370 375			2717
GTG GAG AAG ACG CCT TCT TTG CCA GAT GAC CTC AGT GAC AGT ACC AGC Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser 380 385 390			2765
TTG GGG ACC AGT GTC ATC ACC ACC TGC ACG TCT GTC CAG GAG CAG GGG Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Val Gln Glu Gln Gly 395 400 405			2813
CTG AAG GCC AAC AAC TCC AAA GAG TTA AGC ATG TGC TTC ACA GAG CTC Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu 410 415 420 425			2861
ACG ACA AAT ATC ATC CCA GGG AGT AAC AAG GTG ATC AAA CCT AAC TCA Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser 430 435 440			2909
GGC CCC AGC AGA GCC AGA CCG TCG GCT GCC TTG ACC GTG CTG TCT GTC Gly Pro Ser Arg Ala Arg Pro Ser Ala Ala Leu Thr Val Leu Ser Val 445 450 455			2957
CTG ATG CTG AAA CTG GCC TTG TAGGCTGTGG GAACCGAGTC AGAAGATTTT Leu Met Leu Lys Leu Ala Leu			3008
460			
TGAAAGCTAC GCAGACAAGA ACAGCCGCCT GACGAAATGG AAACACACAC AGACACACAC			3068
ACACCTTGCA AAAAAAAAAAT TGTTTTTCCC ACCTTGTCGC TGAACCTGTC TCCTCCCAGG			3128
TTTCTTCTCT GGAGAAGTTT TTGTAAACCA AACAGACAAG CAGGCAGGCA GCCTGAGAGC			3188
TGGCCCAGGG GTCCCCTGGC AGGGGAAACT CTGGTGCCGG GGAGGGCACG AGGCTCTAGA			3248
AATGCCCTTC ACTTTCTCCT GGTGTTTTTC TCTCTGGACC CTTCTGAAGC AGAGACCGGA			3308
CAAGAGCCTG CAGCGGAAGG GACTCTGGGC TGTGCCTGAG GCTGGCTGGG GGCAGGACAA			3368
CACAGCTGCT TCCCCAGGCT GCCCACTCTG GGGACCCGCT GGGGGCTGGC AGAGGGCATC			3428
GGTCAGCGGG GCAGCGGGG TGGCCATGAG GGTCCACCTT CAGCCCTTTG GCTTCAAGGA			3488
TGGAGATGGT TTTGCCCTCC CTCTCTGCCC TCGGGTGGGG CTGGTGGGTC TGCAGCTGGT			3548
GTGGGAACTT CCCCACGGAT GGCGGTGGAG GGGGTTCGCA CCGTGCTGGG CTCCCCCTGA			3608
CTGTAGCACG GAGTGTGGG GCTGGGGGCC AGCTCCAGGA GGGCTTGAGA GCTCAGCCTG			3668
CCTGGGAGAG CCCTTGTGGC GAGGCATTAA AACTTGGGCA CCAGCTTCTT TCTCGGTGGC			3728
AGAAATTTTG AAGTCAGAGA GAAACGGTCC TTTGTTGGCT TCTTTGCTTT CTCGTGGGTC			3788

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CTTTGGCAGG CCTCCCTTTG GGGAGAGGGA GGGGAGAGAC CACAGCCGGG TGTGTGTCTG      3848
CAGCACCGTG GGCCCTCAAG CTTTCCTGCT GTCTTCTCCC TCCTCCTCCT TTCCCCTTTC      3908
TCTTTCCTCA TTTCCTAGAC GTACGTCAAC TGTATGTACA TACCGGGGCT CCTCTCCTAA      3968
CATATATGTA TATACACATC CATATACATA TATTGTGTGG TTTCCCCTTT CTTTCCTTTT      4028
TTTAAGCAAC AAAACTATGG AAATAATACC CCAACAGATG AGCGAAAATG TATTATTGTA      4088
AAGTTTATTT TTTTAAATAC TGTTGTCTAT AATGGGGAAA AAGGACATTG GCCCCGCAGT      4148
GCCCTGCCCC AGTCAGCCTG GCTGGGCTCT GGTGGGGGCT CCTGATCCGC ATCCAAGCTT      4208
AACCAAGGCT CCAATAAACG TGCG                                          4232

```

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 464 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Asp Thr
 1             5             10             15
Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His
          20             25             30
Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
          35             40             45
Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
          50             55             60
Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
          65             70             75             80
Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
          85             90             95
Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
          100             105             110
His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
          115             120             125
Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
          130             135             140
Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
          145             150             155             160
Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
          165             170             175
Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
          180             185             190

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Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe
		195					200					205			
Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys
	210					215					220				
Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	Pro	Ser
	225				230					235					240
Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Gly
				245					250					255	
Val	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	His
			260					265					270		
Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Gln	Thr	Val	Thr	Ser	Cys	Pro	Ala	Asp
		275					280					285			
Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe	Asp
	290					295					300				
Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	Pro	Thr	Gly	Ile	Val	Val	Ser
	305				310					315					320
Pro	Trp	Cys	Ser	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu
				325					330					335	
Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	Ile
			340					345					350		
Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asn	Val	Asn	Val	Ser	Pro	Lys	Gly	Pro
		355					360					365			
Ser	Phe	Gln	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	Leu
	370					375					380				
Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	Thr
	385				390					395				400	
Thr	Cys	Thr	Ser	Val	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	Lys
				405					410					415	
Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ile	Pro	Gly
			420					425					430		
Ser	Asn	Lys	Val	Ile	Lys	Pro	Asn	Ser	Gly	Pro	Ser	Arg	Ala	Arg	Pro
		435					440					445			
Ser	Ala	Ala	Leu	Thr	Val	Leu	Ser	Val	Leu	Met	Leu	Lys	Leu	Ala	Leu
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 203..1402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAAGTCAAAG GTTTAATCAT GATCCAAGAG CCCAGAGAGA CTTTAGGACA ATAATAGGAA	60
TAAAGCAAGG CCCACAGGCT CCAGCTCCTG ATGCCCAGAT GTTCGGCAGG ATCCGGGGAC	120
AGGGCAGTGC AGGCAGTAGT TTTCCATCCT CCATCCAGGG GAGGAGCGAG GGGAGCGCGG	180
AGCCCGGCGC CTACAGCTCG CC ATG GTG CGC CCC CTG AAC CCG CGA CCG CTG	232
Met Val Arg Pro Leu Asn Pro Arg Pro Leu	
1 5 10	
CCG CCC GTA GTC CTG ATG TTG CTG CTG CTG CTG CCG CCG TCG CCG CTG	280
Pro Pro Val Val Leu Met Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu	
15 20 25	
CCT CTC GCA GCC GGA GAC CCC CTT CCC ACA GAA AGC CGA CTC ATG AAC	328
Pro Leu Ala Ala Gly Asp Pro Leu Pro Thr Glu Ser Arg Leu Met Asn	
30 35 40	
AGC TGT CTC CAG GCC AGG AGG AAG TGC CAG GCT GAT CCC ACC TGC AGT	376
Ser Cys Leu Gln Ala Arg Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser	
45 50 55	
GCT GCC TAC CAC CAC CTG GAT TCC TGC ACC TCT AGC ATA AGC ACC CCA	424
Ala Ala Tyr His His Leu Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro	
60 65 70	
CTG CCC TCA GAG GAG CCT TCG GTC CCT GCT GAC TGC CTG GAG GCA GCA	472
Leu Pro Ser Glu Glu Pro Ser Val Pro Ala Asp Cys Leu Glu Ala Ala	
75 80 85 90	
CAG CAA CTC AGG AAC AGC TCT CTG ATA GGC TGC ATG TGC CAC CGG CGC	520
Gln Gln Leu Arg Asn Ser Ser Leu Ile Gly Cys Met Cys His Arg Arg	
95 100 105	
ATG AAG AAC CAG GTT GCC TGC TTG GAC ATC TAT TGG ACC GTT CAC CGT	568
Met Lys Asn Gln Val Ala Cys Leu Asp Ile Tyr Trp Thr Val His Arg	
110 115 120	
GCC CGC AGC CTT GGT AAC TAT GAG CTG GAT GTC TCC CCC TAT GAA GAC	616
Ala Arg Ser Leu Gly Asn Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp	
125 130 135	
ACA GTG ACC AGC AAA CCC TGG AAA ATG AAT CTC AGC AAA CTG AAC ATG	664
Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser Lys Leu Asn Met	
140 145 150	
CTC AAA CCA GAC TCA GAC CTC TGC CTC AAG TTT GCC ATG CTG TGT ACT	712
Leu Lys Pro Asp Ser Asp Leu Cys Leu Lys Phe Ala Met Leu Cys Thr	
155 160 165 170	
CTC AAT GAC AAG TGT GAC CGG CTG CGC AAG GCC TAC GGG GAG GCG TGC	760
Leu Asn Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys	
175 180 185	
TCC GGG CCC CAC TGC CAG CGC CAC GTC TGC CTC AGG CAG CTG CTC ACT	808
Ser Gly Pro His Cys Gln Arg His Val Cys Leu Arg Gln Leu Leu Thr	
190 195 200	

TTCTCCTTTG TGAAGAAGGC TCCTGCCCCC TCGTCTCCTC CTCTGAGTGG AGGATGGAAA 1852
 ACTACTGCCT GCACTGCCCT GTCCCCGGAT CCTGCCGAAC ATCTGGGCAT CAGGAGCTGG 1912
 AGCCTGTGGG CCTTGCTTTA TTCCTATTAT TGTCTCTAAAG TCTCTCTGGG CTCTTGGATC 1972
 ATGATTAAAC CTTTGACTG 1991

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met	1	5	10	15
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp	20	25	30	
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg	35	40	45	
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu	50	55	60	
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro	65	70	75	
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser	85	90	95	
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala	100	105	110	
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn	115	120	125	
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	130	135	140	
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	145	150	155	
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	165	170	175	
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln	180	185	190	
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala	195	200	205	
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp	210	215	220	
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala				

225	230	235	240
Leu Pro Pro Val	Ala Pro Asn Cys Leu Glu	Leu Arg Arg Leu Cys Phe	
	245	250	255
Ser Asp Pro	Leu Cys Arg Ser Arg	Leu Val Asp Phe Gln Thr	His Cys
	260	265	270
His Pro Met	Asp Ile Leu Gly Thr Cys Ala Thr	Glu Gln Ser Arg Cys	
	275	280	285
Leu Arg Ala Tyr	Leu Gly Leu Ile Gly Thr Ala Met	Thr Pro Asn Phe	
	290	295	300
Ala Ser Asn Val	Asn Thr Ser Val Ala Leu Ser	Cys Thr Cys Arg Gly	
305	310	315	320
Ser Gly Asn Leu	Gln Glu Glu Cys Glu Met	Leu Glu Gly Phe Phe Ser	
	325	330	335
His Asn Pro	Cys Leu Thr Glu Ala Ile Ala Ala	Lys Met Arg Phe His	
	340	345	350
Ser Gln Leu Phe	Ser Gln Asp Trp Pro His Pro Thr	Phe Ala Val Met	
	355	360	365
Ala His Gln Asn	Glu Asn Pro Ala Val Arg Pro Gln	Pro Trp Val Pro	
	370	375	380
Ser Leu Phe Ser	Cys Thr Leu Pro Leu Ile Leu Leu Leu	Ser Leu Trp	
385	390	395	400

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 684..2063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCGGCCGCGT CGACCTTGAC CATGCAGACA CTTTTTCAGG CCTCTGTCTG GTGTGAAGTT	60
GGCAGATACA AGCAAGGCC GAAAGGGGTC TCAGCTTCTC TCTCCTGGGC CTCCTGGACT	120
GAGTTAGGCT TGCTTCTGGT TGTCTTCTAA AGGCACGGTG ATACAGAATG ATGAGACTAG	180
GCTGGAGGGG GCTTTCTGCT TCTCTGTGTG TGACCTTGAG TTATCTCCCT TCGTTGGATC	240
CGAGCTTTCC TGGAATATGA TGTTGAATAT GAATATGAGT TCTGCCTAAG GTCCAGACAG	300
GCTCTGAGGG TTAAGTACT TTTGGAGCCT TCAAATCAAT ACCTTGATG GAGTGGGGGT	360
TTGTCCAATG GGAGTTGAGG CAAGATCCCT TTGCATAAGC CTTGCCACAT CATGTTGAAG	420

CCATGCCATT	CTGTCTGGAC	TATTGGCATC	TTACCTTTCC	AGCAGTTTCA	GTGAAGGCCT	480
TCCTGGATTT	ATCATTTCTGT	GTTCCACTGC	CTAGGATTGT	GCTCAAGAGG	AAATGAATGT	540
GAACCATGGT	TGTAGGGGAG	TATGGCCAAC	CAGGTTGGGT	CTGTGTTGAC	CTTGGTCTTG	600
GTGTTCTTTT	GTGTAAAGTG	GGTGAGAAGT	TCCTTCAAAC	CTTAGGCCTA	CATTGGGGTC	660
AGAGACTGTG	GTGGCCCTCA	TTC	ATG	CTT	GTC	710
		Met	Leu	Val	Phe	
		1			5	
GAC	GAA	ACC	CTC	CGC	TCT	758
Asp	Glu	Thr	Leu	Arg	Ser	
10				15	20	25
GAG	CTC	CAC	GGC	TGG	CGC	806
Glu	Leu	His	Gly	Trp	Arg	
			30		35	40
CTG	TGT	GCG	GCT	GAA	TCC	854
Leu	Cys	Ala	Ala	Glu	Ser	
		45		50	55	
CAG	TGC	CTG	GCA	GGC	CGG	902
Gln	Cys	Leu	Ala	Gly	Arg	
		60		65	70	
TGC	CAG	GCA	GCC	CTG	GAG	950
Cys	Gln	Ala	Ala	Leu	Glu	
	75			80	85	
CGC	TGC	AAG	CGG	GGC	ATG	998
Arg	Cys	Lys	Arg	Gly	Met	
90				95	100	105
TGG	AGC	ATC	CAT	CTG	GGG	1046
Trp	Ser	Ile	His	Leu	Gly	
			110		115	120
TCC	CCC	TAT	GAG	CCT	GTG	1094
Ser	Pro	Tyr	Glu	Pro	Val	
			125		130	135
GCT	TCA	ATC	TTC	TCA	GGG	1142
Ala	Ser	Ile	Phe	Ser	Gly	
		140			145	150
AGC	AAC	CAC	TGC	CTG	GAT	1190
Ser	Asn	His	Cys	Leu	Asp	
	155				160	165
TGC	AAG	AAG	CTT	CGC	TCC	1238
Cys	Lys	Lys	Leu	Arg	Ser	
170				175	180	185
TCT	CCC	ACC	GAA	CGC	TGC	1286
Ser	Pro	Thr	Glu	Arg	Cys	
			190		195	200
CAG	TTC	TTT	GAC	CGT	GTG	1334
Gln	Phe	Phe	Asp	Arg	Val	
			205		210	215

1382
1430
1478
1526
1574
1622
1670
1718
1766
1814
1862
1910
1958
2006
2054
2103

CAGATATGAA CTCCCGCCTG ACAAATGGA AACACACGCA TACACACATG CCACACACAG 2163
 ACACACACAC AGACACACAC ACACACACAC ATACAGACGT CGACGCGGCC GC 2215

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Leu	Val	Phe	Pro	Ser	His	Tyr	Pro	Asp	Glu	Thr	Leu	Arg	Ser	Leu	1	5	10	15
Ala	Ser	Pro	Ser	Ser	Leu	Gln	Gly	Ser	Glu	Leu	His	Gly	Trp	Arg	Pro	20	25	30	
Gln	Val	Asp	Cys	Val	Arg	Ala	Asn	Glu	Leu	Cys	Ala	Ala	Glu	Ser	Asn	35	40	45	
Cys	Ser	Ser	Arg	Tyr	Arg	Thr	Leu	Arg	Gln	Cys	Leu	Ala	Gly	Arg	Asp	50	55	60	
Arg	Asn	Thr	Met	Leu	Ala	Asn	Lys	Glu	Cys	Gln	Ala	Ala	Leu	Glu	Val	65	70	75	80
Leu	Gln	Glu	Ser	Pro	Leu	Tyr	Asp	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	85	90	95	
Lys	Glu	Leu	Gln	Cys	Leu	Gln	Ile	Tyr	Trp	Ser	Ile	His	Leu	Gly	Leu	100	105	110	
Thr	Glu	Gly	Glu	Glu	Phe	Tyr	Glu	Ala	Ser	Pro	Tyr	Glu	Pro	Val	Thr	115	120	125	
Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Leu	Ala	Ser	Ile	Phe	Ser	Gly	Thr	130	135	140	
Gly	Thr	Asp	Pro	Ala	Val	Ser	Thr	Lys	Ser	Asn	His	Cys	Leu	Asp	Ala	145	150	155	160
Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Asn	Cys	Lys	Lys	Leu	Arg	Ser	Ser	165	170	175	
Tyr	Ile	Ser	Ile	Cys	Asn	Arg	Glu	Ile	Ser	Pro	Thr	Glu	Arg	Cys	Asn	180	185	190	
Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Arg	Val	Pro	195	200	205	
Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys	Gln	Asp	Gln	Ala	210	215	220	
Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	Pro	Ser	Cys	Ser	Tyr	Glu	225	230	235	240
Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser	Leu	Cys	Arg	Thr	245	250	255	

Asp	His	Leu	Cys 260	Arg	Ser	Arg	Leu	Ala 265	Asp	Phe	His	Ala	Asn 270	Cys	Arg
Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser 280	Cys	Pro	Ala	Asp	Asn 285	Tyr	Gln	Ala
Cys	Leu	Gly	Ser	Tyr	Ala	Gly 295	Met	Ile	Gly	Phe	Asp 300	Met	Thr	Pro	Asn
Tyr 305	Val	Asp	Ser	Asn	Pro 310	Thr	Gly	Ile	Val	Val 315	Ser	Pro	Trp	Cys	Asn 320
Cys	Arg	Gly	Ser	Gly 325	Asn	Met	Glu	Glu	Glu 330	Cys	Glu	Lys	Phe	Leu 335	Arg
Asp	Phe	Thr	Glu 340	Asn	Pro	Cys	Leu	Arg 345	Asn	Ala	Ile	Gln	Ala 350	Phe	Gly
Asn	Gly	Thr 355	Asp	Val	Asn	Met	Ser 360	Pro	Lys	Gly	Pro	Ser 365	Leu	Pro	Ala
Thr	Gln 370	Ala	Pro	Arg	Val	Glu 375	Lys	Thr	Pro	Ser	Leu 380	Pro	Asp	Asp	Leu
Ser 385	Asp	Ser	Thr	Ser	Leu 390	Gly	Thr	Ser	Val	Ile 395	Thr	Thr	Cys	Thr	Ser 400
Ile	Gln	Glu	Gln	Gly 405	Leu	Lys	Ala	Asn	Asn 410	Ser	Lys	Glu	Leu	Ser 415	Met
Cys	Phe	Thr	Glu 420	Leu	Thr	Thr	Asn	Ile 425	Ser	Pro	Gly	Ser	Lys 430	Lys	Val
Ile	Lys	Leu 435	Asn	Ser	Gly	Ser	Ser 440	Arg	Ala	Arg	Leu	Ser 445	Ala	Ala	Leu
Thr	Ala 450	Leu	Pro	Leu	Leu	Met 455	Leu	Thr	Leu	Ala	Leu 460				

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 67..1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCGGCCGCGT CGACCGACGC CCAGCACAGG CAGAGCGCTG CCGGGTCCGC GCGTCCAGA 60
 CCCGCC ATG GGG CTC TCC CGG AGC CCG CGA CCG CCG CCG CTA GTG ATC 108
 Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile
 1 5 10

CTG Leu 15	CTA Leu	CTG Leu	GTG Val	CTG Leu	TCG Ser 20	CTG Leu	TGG Trp	CTA Leu	CCC Pro	CTT Leu 25	GGA Gly	ACA Thr	GGA Gly	AAC Asn	TCC Ser 30	156
CTT Leu	CCC Pro	ACA Thr	GAG Glu	AAC Asn 35	AGG Arg	CTT Leu	GTG Val	AAC Asn	AGC Ser 40	TGT Cys	ACC Thr	CAG Gln	GCC Ala	AGA Arg 45	AAA Lys	204
AAA Lys	TGC Cys	GAG Glu	GCT Ala 50	AAT Asn	CCC Pro	GCT Ala	TGC Cys	AAG Lys 55	GCT Ala	GCC Ala	TAC Tyr	CAG Gln	CAC His 60	CTG Leu	GAC Asp	252
TCC Ser	TGC Cys	ACC Thr 65	CCC Pro	AGT Ser	CTC Leu	AGC Ser	AGT Ser 70	CCA Pro	CTG Leu	CCC Pro	TCA Ser	GGG Gly 75	GAG Glu	TCT Ser	GCC Ala	300
ACA Thr 80	TCT Ser	GCA Ala	GCG Ala	TGC Cys	CTT Leu	GAA Glu 85	GCA Ala	GCA Ala	CAG Gln	CAA Gln	CTC Leu 90	AGG Arg	AAC Asn	AGC Ser	TCT Ser	348
CTC Leu 95	ATA Ile	GAC Asp	TGC Cys	AGG Arg	TGC Cys 100	CAC His	CGG Arg	CGC Arg	ATG Met	AAG Lys 105	CAC His	CAA Gln	GCT Ala	ACC Thr	TGT Cys 110	396
CTG Leu	GAC Asp	ATT Ile	TAT Tyr	TGG Trp 115	ACC Thr	GTT Val	CAC His	CCT Pro	GTC Val 120	CGA Arg	AGC Ser	CTT Leu	GGT Gly	GAC Asp 125	TAC Tyr	444
GAG Glu	TTG Leu	GAC Asp	GTC Val 130	TCA Ser	CCC Pro	TAT Tyr	GAA Glu	GAC Asp 135	ACA Thr	GTG Val	ACC Thr	AGC Ser	AAA Lys 140	CCC Pro	TGG Trp	492
AAA Lys	ATG Met	AAT Asn 145	CTC Leu	AGC Ser	AAG Lys	CTG Leu	AGC Ser 150	ATG Met	CTC Leu	AAA Lys	CCA Pro	GAC Asp 155	TCC Ser	GAC Asp	CTC Leu	540
TGC Cys 160	CTC Leu	AAA Lys	TTT Phe	GCT Ala	ATG Met	CTG Leu 165	TGT Cys	ACT Thr	CTT Leu	AAC Asn	GAC Asp 170	AAG Lys	TGC Cys	GAC Asp	CGC Arg	588
CTC Leu 175	CGA Arg	AAG Lys	GCC Ala	TAC Tyr	GGG Gly 180	GAG Glu	GCG Ala	TGC Cys	TCA Ser	GGG Gly 185	ATC Ile	CGC Arg	TGC Cys	CAG Gln	CGC Arg 190	636
CAC His	CTC Leu	TGC Cys	CTA Leu	GCT Ala 195	CAG Gln	CTG Leu	CGC Arg	TCC Ser	TTC Phe 200	TTC Phe	GAG Glu	AAG Lys	GCG Ala	GCA Ala 205	GAG Glu	684
TCC Ser	CAC His	GCT Ala	CAG Gln 210	GGC Gly	CTG Leu	CTG Leu	CTG Leu	TGT Cys 215	CCC Pro	TGT Cys	GCA Ala	CCC Pro	GAA Glu 220	GAT Asp	GCG Ala	732
GGC Gly	TGT Cys	GGG Gly 225	GAG Glu	CGC Arg	CGG Arg	CGC Arg	AAC Asn 230	ACC Thr	ATC Ile	GCC Ala	CCC Pro	AGT Ser 235	TGC Cys	GCC Ala	CTC Leu	780
CCG Pro	TCT Ser 240	GTG Val	GCC Ala	CCC Pro	AAC Asn	TGC Cys 245	CTA Leu	GAT Asp	CTT Leu	CGG Arg	AGC Ser 250	TTC Phe	TGC Cys	CGT Arg	GCG Ala	828
GAC Asp 255	CCT Pro	CTG Leu	TGC Cys	AGA Arg	TCA Ser 260	CGC Arg	CTG Leu	ATG Met	GAC Asp	TTC Phe 265	CAG Gln	ACC Thr	CAC His	TGC Cys	CAC His 270	876

(2) INFORMATION FOR SEQ ID NO:42:

(A) LENGTH: 397 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile Leu Leu
1 5 10 15

Leu Val Leu Ser Leu Trp Leu Pro Leu Gly Thr Gly Asn Ser Leu Pro

20					25					30					
Thr	Glu	Asn	Arg	Leu	Val	Asn	Ser	Cys	Thr	Gln	Ala	Arg	Lys	Lys	Cys
		35					40					45			
Glu	Ala	Asn	Pro	Ala	Cys	Lys	Ala	Ala	Tyr	Gln	His	Leu	Asp	Ser	Cys
	50					55					60				
Thr	Pro	Ser	Leu	Ser	Ser	Pro	Leu	Pro	Ser	Gly	Glu	Ser	Ala	Thr	Ser
65					70					75					80
Ala	Ala	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile
				85					90					95	
Asp	Cys	Arg	Cys	His	Arg	Arg	Met	Lys	His	Gln	Ala	Thr	Cys	Leu	Asp
			100					105					110		
Ile	Tyr	Trp	Thr	Val	His	Pro	Val	Arg	Ser	Leu	Gly	Asp	Tyr	Glu	Leu
	115						120					125			
Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met
	130					135					140				
Asn	Leu	Ser	Lys	Leu	Ser	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu
145					150					155					160
Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	Arg	Leu	Arg
				165					170					175	
Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Ile	Arg	Cys	Gln	Arg	His	Leu
			180					185					190		
Cys	Leu	Ala	Gln	Leu	Arg	Ser	Phe	Phe	Glu	Lys	Ala	Ala	Glu	Ser	His
		195					200					205			
Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Glu	Asp	Ala	Gly	Cys
	210					215					220				
Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Ser	Cys	Ala	Leu	Pro	Ser
225					230					235					240
Val	Ala	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser	Phe	Cys	Arg	Ala	Asp	Pro
				245					250					255	
Leu	Cys	Arg	Ser	Arg	Leu	Met	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met
			260				265						270		
Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala
	275						280					285			
Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Ile	Ser	Lys
	290					295					300				
Val	Asn	Thr	Thr	Val	Ala	Leu	Gly	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn
305					310					315					320
Leu	Gln	Asp	Glu	Cys	Glu	Gln	Leu	Glu	Lys	Ser	Phe	Ser	Gln	Asn	Pro
				325					330					335	
Cys	Leu	Met	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Arg	Gln	Leu
			340					345					350		
Phe	Ser	Gln	Asp	Trp	Ala	Asp	Ser	Thr	Phe	Ser	Val	Met	Gln	Gln	Gln
		355					360					365			

157k
168

Asn Ser Ser Pro Ala Leu Arg Pro Gln Leu Arg Leu Pro Val Leu Ser
370 375 380

Phe Phe Ile Leu Thr Leu Ile Leu Leu Gln Thr Leu Trp
385 390 395

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Val	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Pro	Xaa	Pro	Pro	Xaa	Xaa	Xaa	Met	1	5	10	15
Xaa	Leu	Xaa	Leu	Leu	Ser	Leu	Ala	Leu	Pro	Leu	Xaa	Xaa	Xaa	Leu	Gln	20	25	30	
Gly	Ala	Glu	Leu	Xaa	Gly	Xaa	Xaa	Arg	Leu	Xaa	Xaa	Asp	Cys	Val	Xaa	35	40	45	
Ala	Xaa	Xaa	Xaa	Cys	Xaa	Ala	Glu	Xaa	Xaa	Cys	Ser	Xaa	Xaa	Tyr	Arg	50	55	60	
Thr	Leu	Arg	Gln	Cys	Xaa	Ala	Gly	Xaa	Xaa	Xaa	Asn	Thr	Xaa	Leu	Ala	65	70	75	80
Ser	Gly	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Ala	Xaa	Glu	85	90	95	
Xaa	Leu	Xaa	Xaa	Ser	Ser	Leu	Tyr	Asp	Cys	Arg	Cys	Lys	Arg	Gly	Met	100	105	110	
Lys	Lys	Glu	Xaa	Xaa	Cys	Leu	Xaa	Ile	Tyr	Trp	Ser	Xaa	His	Xaa	Xaa	115	120	125	
Leu	Xaa	Xaa	Gly	Asn	Xaa	Xaa	Leu	Glu	Xaa	Ser	Pro	Tyr	Glu	Pro	Xaa	130	135	140	
Val	Thr	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Xaa	Xaa	Ser	Xaa	Xaa	Ser	145	150	155	160
Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Ser	Asn	Xaa	Cys	Leu	165	170	175	
Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Xaa	Cys	Lys	Lys	Leu	Arg	180	185	190	
Ser	Ala	Tyr	Ile	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Glu	Arg	195	200	205	
Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	210	215	220	

Val	Pro	Xaa	Xaa	His	Xaa	Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Xaa	Xaa
225					230					235					240
Xaa	Asp	Xaa	Ala	Cys	Xaa	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Xaa	Pro	Ser
				245					250					255	
Cys	Ser	Tyr	Glu	Xaa	Xaa	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Xaa
			260					265					270		
Xaa	Cys	Arg	Thr	Asp	Xaa	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	Xaa
		275					280					285			
Thr	Asn	Cys	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Val	Xaa	Ser	Cys	Xaa	Ala	Xaa
	290					295					300				
Asn	Tyr	Xaa	Xaa	Cys	Leu	Xaa	Ala	Tyr	Xaa	Gly	Leu	Ile	Gly	Thr	Xaa
305					310					315					320
Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	Xaa	Thr	Xaa	Xaa	Xaa	Val	Ala
				325					330					335	
Pro	Trp	Cys	Xaa	Cys	Arg	Gly	Ser	Gly	Asn	Xaa	Xaa	Glu	Glu	Cys	Glu
			340					345					350		
Lys	Phe	Leu	Xaa	Phe	Phe	Xaa	Xaa	Asn	Pro	Cys	Leu	Xaa	Asn	Ala	Ile
		355					360					365			
Gln	Ala	Phe	Gly	Asn	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	370					375						380			
Xaa	Pro	Xaa	Phe	Ser	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Thr	Xaa	Ala
385					390					395					400
Xaa	Arg	Val	Xaa	Xaa	Xaa	Pro	Ser	Leu	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa
				405					410					415	
Xaa	Xaa	Leu	Xaa	Thr	Xaa	Val	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Leu	Gln	Xaa
			420					425					430		
Gln	Xaa	Leu	Lys	Xaa	Asn	Xaa	Ser	Xaa	Glu	Xaa	Xaa	Xaa	Cys	Phe	Xaa
		435					440					445			
Glu	Leu	Thr	Thr	Asn	Xaa	Xaa	Xaa	Xaa	Ser	Gly	Xaa	Xaa	Xaa	Xaa	Ile
	450					455					460				
Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Ala	Xaa	Pro	Ser	Xaa	Ala	Leu	Xaa	Xaa	Leu
465					470					475					480
Pro	Val	Leu	Met	Leu	Thr	Ala	Leu	Ala	Xaa	Leu	Leu	Ser	Xaa	Xaa	Xaa
				485					490					495	

Xaa Ser

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Leu	Xaa
1				5					10					15	
Thr	Leu	Xaa	Ser	Leu	Xaa	Xaa	Pro	Leu	Xaa	Leu	Xaa	Xaa	Ser	Xaa	Xaa
			20					25					30		
Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	Asp	Cys	Val	Xaa	Ala	Xaa	Xaa	Xaa	Cys
			35				40					45			
Xaa	Ala	Glu	Xaa	Xaa	Cys	Ser	Xaa	Xaa	Tyr	Arg	Thr	Leu	Arg	Gln	Cys
	50					55					60				
Xaa	Ala	Gly	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala
65					70					75					80
Xaa	Xaa	Glu	Cys	Xaa	Xaa	Ala	Xaa	Glu	Xaa	Leu	Xaa	Xaa	Ser	Ser	Leu
				85				90						95	
Tyr	Asp	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Xaa	Xaa	Cys	Leu
			100					105						110	
Xaa	Ile	Tyr	Trp	Ser	Xaa	His	Xaa	Xaa	Leu	Xaa	Xaa	Gly	Xaa	Xaa	Xaa
		115					120					125			
Leu	Glu	Xaa	Ser	Pro	Tyr	Glu	Xaa	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp
	130					135					140				
Ile	Phe	Arg	Xaa	Xaa	Ser	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa
145					150					155					160
Xaa	Xaa	Xaa	Lys	Ser	Asn	Xaa	Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn
				165					170					175	
Leu	Asn	Asp	Xaa	Cys	Lys	Lys	Leu	Arg	Ser	Ala	Tyr	Ile	Xaa	Xaa	Cys
			180					185					190		
Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His
			195				200					205			
Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Xaa	Xaa	His	Xaa	Tyr
	210				215						220				
Gly	Met	Leu	Phe	Cys	Ser	Cys	Xaa	Xaa	Xaa	Asp	Xaa	Ala	Cys	Xaa	Glu
225					230					235					240
Arg	Arg	Arg	Gln	Thr	Ile	Xaa	Pro	Ser	Cys	Ser	Tyr	Glu	Xaa	Xaa	Glu
				245					250					255	
Xaa	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser	Xaa	Cys	Arg	Thr	Asp	Xaa	Leu
			260					265					270		
Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	Xaa	Thr	Asn	Cys	Xaa	Pro	Xaa	Xaa
		275					280					285			
Arg	Xaa	Xaa	Thr	Xaa	Cys	Xaa	Ala	Xaa	Asn	Tyr	Xaa	Xaa	Cys	Leu	Xaa
	290					295					300				
Ala	Tyr	Xaa	Gly	Leu	Ile	Gly	Thr	Xaa	Met	Thr	Pro	Asn	Tyr	Val	Asp
305					310					315					320

Ser Xaa Xaa Thr Xaa Xaa Xaa Val Ala Pro Trp Cys Xaa Cys Arg Gly
325 330 335

Ser Gly Asn Xaa Xaa Glu Glu Cys Glu Lys Phe Leu Xaa Xaa Phe Xaa
340 345 350

Xaa Asn Pro Cys Leu Xaa Asn Ala Ile Gln Ala Phe Gly Asn Gly Xaa
355 360 365

Asp Val Xaa Met Ser Gln Xaa Xaa Pro Xaa Xaa Xaa Xaa Thr Xaa Ala
370 375 380

Xaa Xaa Xaa Xaa Xaa Xaa Arg Val Xaa Xaa Xaa Pro Xaa Leu Xaa Xaa
385 390 395 400

Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Val Xaa Xaa Xaa Cys
405 410 415

Xaa Xaa Xaa Gln Xaa Gln Xaa Leu Lys Xaa Asn Xaa Ser Xaa Xaa Xaa
420 425 430

Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
435 440 445

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Ala Xaa Xaa Ser Xaa
450 455 460

Xaa Leu Xaa Xaa Leu Pro Val Leu Met Leu Thr Xaa Leu Xaa Xaa Xaa
465 470 475 480

Leu Xaa Xaa Xaa Leu Xaa Glu Thr Ser
485

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